

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 20:38:13 ; Search time 304 Seconds

(without alignments)
7511.600 Million cell updates/sec

Title: US-10-023-775b-1

Perfect score: 1014
Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

- 1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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- 20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1014	100.0	1014	24	ABQ78847 Human G-protein co
2	1014	100.0	1014	24	AAD34278 Human AXOR89 (G-pr
3	1014	100.0	1014	24	AAD26370 Human G-protein co
4	1012.4	99.8	1014	22	AA507948 Human cDNA encodin
5	1012.4	99.8	1014	24	ABR85630 Human P2Y-like rec
6	1012.4	99.8	1014	24	ABR11381 Human DNA encoding
7	1012.4	99.8	1014	24	AAK98323 Human purinergic-r
8	1012.4	99.8	1288	24	ABU56197 Human P2Y1-1l enco
9	1012.4	99.8	5435	24	ABU56198 Human P2Y1-1l enco

10	1012.4	99.8	9905	24	AAK98324 Human purinergic-r
11	1010.8	99.7	1729	22	AA508362 Human cDNA encodin
12	1010.8	99.7	1729	23	ABY24026 Human prostate exp
13	1010.8	99.7	1729	23	ABY25767 Human prostate exp
14	1010.8	99.7	1729	23	ABY29909 Human prostate exp
15	1010.8	99.7	1729	23	ABY30024 Human prostate exp
16	1009.4	99.5	1011	24	AA439442 Human G-protein-co
17	976.2	96.3	1020	22	AA451011 Human ngPCR54 codi
18	829.4	81.8	831	24	ABN85629 Human P2Y-like rec
19	728	71.8	1313	22	AAK52430 Human polynucleoti
20	560.8	55.3	740	23	ABY15662 Human prostate exp
21	537.2	53.0	578	22	AAH50998 Human ngPCR54 codi
22	481.4	47.5	545	22	ABA08326 Human P2Y purinoc
23	481.4	47.5	545	22	AAK53414 Human polynucleoti
24	426.2	42.0	539	23	ABY39127 Human prostate exp
25	426.2	42.0	539	23	ABY45465 Human prostate exp
26	343.4	33.9	478	23	ABY15479 Human prostate exp
27	341.4	33.7	426	23	ABY36271 Human prostate exp
28	341.4	33.7	426	23	ABY45310 Human prostate exp
29	338.2	33.4	442	23	ABY08973 Human prostate exp
30	332	32.7	2245	24	ABK11380 Human P2Y1-like G
31	322	31.8	435	23	ABY06310 Human prostate exp
32	189	18.6	657	22	AAK50831 Human cDNA encodin
33	149.4	14.7	6721	24	AA518600 Purinergic recepto
34	148.6	14.7	6721	24	AA518599 Purinergic recepto
35	136	13.4	1428	18	AA775146 Human ATP receptor
36	129.6	12.8	1005	21	AAAD01135 Human orphan G pro
37	129.6	12.8	1005	21	AAK46036 Human G-protein co
38	129.6	12.8	1436	24	ABU50790 Human polynucleoti
39	129.6	12.8	1542	24	AAD24958 Human G-protein co
40	127.4	12.6	8423	24	ABU33407 Human immune syste
41	127.4	12.6	1385	21	AAK81122 Human secreted pro
42	127.4	12.6	1996	18	AA771900 Human purinergic r
43	125	12.3	1543	24	ABK12937 DNA sequence of mo
44	121.4	12.0	1429	18	AA774321 Human P2Y4 recepto
45	108.2	10.7	1163	22	AAD04981 Human purinergic r

ALIGNMENTS

RESULT 1	ABQ78847	standard; cDNA; 1014 BP.
ID	ABQ78847;	
AC	ABQ78847;	
XX		
DT	04-OCT-2002 (first entry)	
XX		
DE	Human G-protein coupled receptor P2Y-019 cDNA.	
XX		
KW	Human; G-protein coupled receptor; GPCR; P2Y-019; neuroprotective;	
KW	anti-inflammatory; cytosolic; cardiovascular; anti-allergic; hypotensive;	
KW	anti-atherosclerotic; osteopathic; hypertension; asthma;	
KW	atherosclerosis; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1014
FT		/*tag- a
FT		/product= "P2Y-019"
XX		
PN	EP1219638-A2.	
XX		
PD	03-JUL-2002.	
XX		
PF	04-DEC-2001; 2001EP-0310136.	
XX		
PR	18-DEC-2000; 2000GB-0030854.	
PR	04-MAY-2001; 2001GB-0011031.	
XX		
PA	(PFI2) PFIZER LTD.	

PS Claim 5; Page 111-112; 115pp; English.

The invention relates to human G-protein coupled receptor (GPCR). Polypeptides and polynucleotides, GPCR polypeptides are useful for screening compounds that modulate their activity. They are useful in the diagnosis, prevention and treatment of disorders which include cell proliferative disorders such as arteriosclerosis, hepatitis, myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia, lymphoma; neurological disorders such as epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia, Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia, cardiovascular disorders such as arteriovenous fistula, atherosclerosis, hypertension, vascular tumours, myocardial infarction, hypertensive heart disease, infective endocarditis, cardiomyopathy, myocarditis; gastrointestinal disorders such as dysphagia, peptic oesophagitis, emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea, constipation, acquired immune deficiency syndrome (AIDS), hepatic encephalopathy; autoimmune/inflammatory disorders such as Addison's disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, uveitis, viral, bacterial, fungal, parasitic, protozoal and helminthic infections and trauma; metabolic disorders such as diabetes, obesity and osteoporosis; and viral infections such as infection caused by viral agent classified as adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are useful as probes for assessing toxicity of test compounds. They are also used in gene therapy. The present sequence is human G-protein coupled receptor 2 (GCR2-2) cDNA.

Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match	100.0%	Score 1014:	DB 24:	Length 1014:
Best Local Similarity	100.0%:	Pred. No. 7.1e-285:		
Matches 1014, Conservative	0:	Mismatches 0:	Indels 0:	Gaps 0:

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Db	1	ATGATGAGGCCACTGACGACTATTAGCAAAATGCTTCGATTTTCCCGCATTTATGAGCGCTGCT	60
OY	61	TTTGGAAATTTGACAGATGAAAAACATCCACACAGATGACGACTACCTCCCTGTTATTATAT	120
Db	61	TTTGGAAATTTGACAGATGAAAAACATCCACGTCAGATGACGACTACCTCCCTGTTATTAT	120
OY	121	GGCATTAATCTTCCTCGTGCGGATTTTCCAGGCAATGCAATGCAATATACCAATTACATTTTC	180
Db	121	GGCATTAATCTTCCTCGTGCGGATTTTCCAGGCAATGCAATGCAATATACCAATTACATTTTC	180
OY	181	AAATGAGACCTTGGANAGACAGACACCATCATTTATGCTGTAACCTGGCGACAGATCTTG	240
Db	181	AAATGAGACCTTGGANAGACAGACACCATCATTTATGCTGTAACCTGGCGACAGATCTTG	240
OY	241	CTGTATCTGACACGAGCTCCCTTCCTCGATTCACTACTATATGCCAGTGGGCAAACTGGATC	300
Db	241	CTGTATCTGACACGAGCTCCCTTCCTCGATTCACTACTATATGCCAGTGGGCAAACTGGATC	300
OY	301	TTTGAGAGATTTCATGCTGTAGTTTATATCCGCTTCAGCTTCATTTCAACCGTGTATACAGC	360
Db	301	TTTGAGAGATTTCATGCTGTAGTTTATATCCGCTTCAGCTTCATTTCAACCGTGTATACAGC	360
OY	361	ATCCTCTTCTCACCTGTTTTCAGACATCTTCGCTACTGTGTATTCATTCACCCCAATGAGC	420
Db	361	ATCCTCTTCTCACCTGTTTTCAGACATCTTCGCTACTGTGTATTCATTCACCCCAATGAGC	420
OY	421	TGCTTTTCCATTCACAAAACTCGATGTGCAATTTGAGCTGTGCTGTGGTGTGATCATTT	480
Db	421	TGCTTTTCCATTCACAAAACTCGATGTGCAATTTGAGCTGTGCTGTGGTGTGATCATTT	480
OY	481	TCACGTGTAGCTGTATTCGCCATGATGACCTTCGTATACATTCACAACCAACGACCAACAGA	540
Db	481	TCACGTGTAGCTGTATTCGCCATGATGACCTTCGTATACATTCACAACCAACGACCAACAGA	540

OY		541	TCAGCCTGCTCGACTTACCAAGTTGGATGAATCAATATTAAAGGTACAACCTA	600
Db		541	TCAGCCTGCTCGACTTACCAAGTTGGATGAATCAATATTAAAGGTACAACCTA	600
OY		601	ATTATTGACGCACAACACTTTCTGCCTCCCTTGSGATAGTACACTTTTGCTATACCAG	660
Db		601	ATTATTGACGCACAACACTTTCTGCCTCCCTTGSGATAGTACACTTTTGCTATACCAG	660
OY		661	ATTATTCACACACTGTGACCCCATGAGCTGCAAACCTGACAGCTGCCCTTAAGCAGAAAGCACGA	720
Db		661	ATTATTCACACACTGTGACCCCATGAGCTGCAAACCTGACAGCTGCCCTTAAGCAGAAAGCACGA	720
OY		721	AGGCTAACCACTTCTGCTACTCCTTGATTTTACGATATGTTTTTAAACCTCCATATCTGG	780
Db		721	AGGCTAACCACTTCTGCTACTCCTTGATTTTACGATATGTTTTTAAACCTCCATATCTGG	780
OY		781	AGGTCATTCGGATGGAATCTGCGCGCTTCAANTCAGTTGTTCCATTGAGAATCAGATC	840
Db		781	AGGTCATTCGGATGGAATCTGCGCGCTTCAANTCAGTTGTTCCATTGAGAATCAGATC	840
OY		841	CATGAAGCTTACATCGTTTCTTAGACCATTTAGCTGCTCTGTAAGACACCTTTGGTAACCTGTTA	900
Db		841	CATGAAGCTTACATCGTTTCTTAGACCATTTAGCTGCTCTGTAAGACACCTTTGGTAACCTGTTA	900
OY		901	CTATATGTGTGTGTGTGTCAGCGACAACCTTTCAGCAGGCTGTCTGCTCAACAGTGGATGCCAA	960
Db		901	CTATATGTGTGTGTGTGTCAGCGACAACCTTTCAGCAGGCTGTCTGCTCAACAGTGGATGCCAA	960
OY		961	GTAACGCGGGAACCTTGAGCAGACAAGAAATAATTAGTTACTCAAAACAACCTTTGA	1014
Db		961	GTAACGCGGGAACCTTGAGCAGACAAGAAATAATTAGTTACTCAAAACAACCTTTGA	1014
 RESULT 4 AAS07948 ID AAS07948 standard; cDNA; 1014 BP.				
XX		AAS07948;		
AC		23-OCT-2001 (first entry)		
XX				
DT				
XX				
DE		Human cdna encoding G-protein coupled receptor, hrUP21.		
KW		Human; G-protein coupled receptor; GPCR; hrUP21; agonist;		
XX		inverse agonist; lung cancer; ss.		
OS		Homo sapiens.		
XX				
FH	key	Location/Qualifiers		
FT	CDS	1..1014		
FT		/*tag= "a		
FT		/product= "hrUP21"		
XX				
PN		WO200136471-A2.		
XX				
PD		25-MAY-2001.		
PF		16-NOV-2000; 2000MO-US31509.		
XX				
PR		17-NOV-1999; 99US-0166088.		
PR		17-NOV-1999; 99US-0166099.		
PR		17-NOV-1999; 99US-0166369.		
PR		23-DEC-1999; 99US-0171900.		
PR		23-DEC-1999; 99US-0171901.		
PR		23-DEC-1999; 99US-0171902.		
PR		11-FEB-2000; 2000US-0181749.		
PR		14-MAR-2000; 2000US-0189258.		
PR		14-MAR-2000; 2000US-0189259.		
PR		10-APR-2000; 2000US-0195898.		
PR		10-APR-2000; 2000US-0195899.		
PR		10-APR-2000; 2000US-0196078.		
PR		28-APR-2000; 2000US-0200419.		
PR		12-MAY-2000; 2000US-0203630.		

PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Dang HF, Lowitz KP;
 XX
 DR WPI; 2001-355616/37.
 DR P-PSDB; AAU04375.
 XX
 XX
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX
 PS Claim 55; Page 113-114; 159pp; English.
 XX
 CC The sequence encodes a human G-protein coupled receptor (GPCR),
 CC hGPR1. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX
 SO Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 22; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTATGATTTAGCAAAATGCTTCTGATTTCCCGCATTTAGCAGCTGCT 60
 DB 1 ATGAATGAGCCACTATGATTTAGCAAAATGCTTCTGATTTCCCGCATTTAGCAGCTGCT 60
 QY 61 TTGGAAATGACGATGATGAAACATCCCACTCAAGATGACATCCCTGTTATTTAT 120
 DB 61 TTGGAAATGACGATGATGAAACATCCCACTCAAGATGACATCCCTGTTATTTAT 120
 QY 121 GGCATTATCTTCTCTGCGGATTTCCAGGCAATGAGTAGATTCACCTTACATTTTC 180
 DB 121 GGCATTATCTTCTCTGCGGATTTCCAGGCAATGAGTAGATTCACCTTACATTTTC 180
 QY 181 AAAATGAGACCTTGGAAGAGACGACACATCATTTATGCTGAACTGGCCCTGCAAGATCTG 240
 DB 181 AAAATGAGACCTTGGAAGAGACGACACATCATTTATGCTGAACTGGCCCTGCAAGATCTG 240
 QY 241 CTGTATCTGACGACCTCCCTCTCTGATTCACCTATGATGAGGCGAAGATGATC 300
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 QY 301 TTGGAGATTTCACTGTGTAAGTTATCCGCTCAGCTTCACCTTCAACCTGTATACGAGC 360
 DB 301 TTGGAGATTTCACTGTGTAAGTTATCCGCTCAGCTTCACCTTCAACCTGTATACGAGC 360
 QY 361 ATCCCTCTCTGACCTGTTTCAAGATCTCCGCTATGCTGATTCATTCACCAAGAGC 420
 DB 361 ATCCCTCTCTGACCTGTTTCAAGATCTCCGCTATGCTGATTCATTCACCAAGAGC 420
 QY 421 TGGTTTCATTCACAAATCAGATGAGTGTGAGCTGTGCTGTGATGATCAT 480
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 QY 481 TCACCTGGTAGCTGTCTATTCGATGATGACCTTCTTGATCATCAACCAAGAGCAACAG 540
 DB 481 TCACCTGGTAGCTGTCTATTCGATGATGACCTTCTTGATCATCAACCAAGAGCAACAG 540

QY 541 TCAGCCTGTCTGACACCTCACCAGTTCGATGAACTCAATCTAATTAAGTACAACTTA 600
 DB 541 TCAGCCTGTCTGACACCTCACCAGTTCGATGAACTCAATCTAATTAAGTACAACTTA 600
 QY 601 ATTTGACCTCAACTACTTCTGCTCCCTGCTGGTGTAGTGAACACTTTCCTATACACG 660
 DB 601 ATTTGACCTCAACTACTTCTGCTCCCTGCTGGTGTAGTGAACACTTTCCTATACACG 660
 QY 661 ATTATCCACCTCTGACCCCATGAGCTGCAAACTGACAGCTGCTTAAGCAAGACGCA 720
 DB 661 ATTATCCACCTCTGACCCCATGAGCTGCAAACTGACAGCTGCTTAAGCAAGACGCA 720
 QY 721 AGGCTAACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 721 AGGCTAACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 781 AGGCTAACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 781 AGGCTAACCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 841 CATGAGCTTACATCGTTTCTAGACATTAAGTCTGCTGCAACCTTTGTTAACTGTTA 900
 DB 841 CATGAGCTTACATCGTTTCTAGACATTAAGTCTGCTGCAACCTTTGTTAACTGTTA 900
 QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 GTAAGCGGGAACCTTGTGAGCAAGCAAAATTAAGTACTCAAAACACCTTGA 1014
 DB 961 GTAAGCGGGAACCTTGTGAGCAAGCAAAATTAAGTACTCAAAACACCTTGA 1014

RESULT 5
 ABN85630
 ID ABN85630 standard; DNA; 1014 BP.

AC ABN85630;
 XX
 XX 18-SEP-2002 (first entry)
 XX
 DE Human P2Y-1-like receptor variant encoding gene SEQ ID NO 3.
 XX
 KW Human; P2Y-1-like receptor; HIRPDM 0000037; immunity; inflammation;
 KW cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
 KW immunomodulator; anti-inflammatory; cytostatic; antiallergic;
 KW gastrointestinal; anti-ulcer; antihypertensive; antidiabetic; antitumor;
 KW antibacterial; immunosuppressive; dermatological; nephrotoxic;
 KW antiallergic; analgesic; receptor; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag- a
 FT /product- "P2Y-1-like receptor variant"
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 PN GB2369364-A.
 PD 29-MAY-2002.
 XX
 PF 31-AUG-2001; 2001GB-0021215.
 XX
 PR 01-SEP-2000; 2000GB-0021524.
 PR 06-SEP-2000; 2000GB-0021894.
 PR 25-SEP-2000; 2000GB-0023444.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Food & Drug Admin.
 XX
 WPI; 2002-511268/55.

PT be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 XX
 PS Claim 1, Fig 5, 118pp: English.

XX
 CC The invention relates to a purified human P2Y₁-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y₁-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence encodes the P2Y₁-like GPCR of the invention.

XX
 SQ Sequence 1014 BP, 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTGACTATTATGACAAATGCTTCTGATTTCCCGGATATGACGCTGCT 60
 DB 1 ATGAATGAGCCACTGACTATTATGACAAATGCTTCTGATTTCCCGGATATGACGCTGCT 60
 QY 61 TTGGAAATGACGATGATAAATCCACATGAGATGATGATGATGATGATGATGATGATGAT 120
 DB 61 TTGGAAATGACGATGATAAATCCACATGAGATGATGATGATGATGATGATGATGATGAT 120
 QY 121 GGCATTATCTTCCTGCTGGGATTTCCAGGCAATGAGATGATGATGATGATGATGATGAT 180
 DB 121 GGCATTATCTTCCTGCTGGGATTTCCAGGCAATGAGATGATGATGATGATGATGATGAT 180
 QY 181 AAAATGAGACCTTGGAGAAGACGACACATCATTTATGCTGACCTGGCTGCACAGATCTG 240
 DB 181 AAAATGAGACCTTGGAGAAGACGACACATCATTTATGCTGACCTGGCTGCACAGATCTG 240
 QY 241 CGTGATCTGACAGGCTCCCTCTGATCTACTATGACAGAGTGGGCAAAATCGGATC 300
 DB 241 CGTGATCTGACAGGCTCCCTCTGATCTACTATGACAGAGTGGGCAAAATCGGATC 300
 QY 301 TTGGAGATTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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 DB 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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QY 601 ATTTGACGTGCAACTCTTTCGCTCCCTCCCTGGTATGATGATGATGATGATGATGATGAT 660
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 DB 781 AGGCTATCTGCAATCTGCGCTGCTTCAATGATGATGATGATGATGATGATGATGATGAT 840
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 DB 841 CATGAAGCTTACATCTTCTAGACCATTAAGCTGCTGTAACACCTTTGTAACCTGTTA 900
 QY 901 CTATATGCTGTGCTGACGACAACTTTGACAGGCTGCTGCTCAACAGTGAATGCAAA 960
 DB 901 CTATATGCTGTGCTGACGACAACTTTGACAGGCTGCTGCTCAACAGTGAATGCAAA 960
 QY 961 GTAAGGGGAGACCTTGAGCAAGCAAAATTAATGATGATGATGATGATGATGATGATGAT 1014
 DB 961 GTAAGGGGAGACCTTGAGCAAGCAAAATTAATGATGATGATGATGATGATGATGATGAT 1014

RESULT 7
 AAK98323
 ID AAK98323 standard; cDNA; 1014 BP.

XX AAK98323;

XX 30-APR-2002 (first entry)

XX Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.

XX Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;

XX signal transduction; human protein; GPCR disorder; gene therapy;

XX transgenic animal; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1014

XX FT /tag="a

XX FT /product="G-protein coupled receptor"

XX WO200187980-A2.

XX 22-NOV-2001.

XX 17-MAY-2001; 2001WO-US15957.

XX 18-MAY-2000; 2000US-205196P.

XX 08-AUG-2000; 2000US-0634656.

XX (APPL-) APPLERA CORP.

XX Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;

XX WPI; 2002-075312/10.

XX P-PSDB; AAO14027.

XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterised by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies
 PS Claim 23; Fig 1; 64pp: English.

CC etc., are used for diagnosis and (gene) therapy of diseases that are
 CC (indirectly associated with (I) or its expression products. No diseases
 CC are specified but as (I) is expressed only in thyroid tissue, (I) is
 CC presumed to be involved in regulation of thyroid function. The present
 CC sequence is that of the P2Y11 encoding cDNA.

XX Sequence 1288 BP; 347 A; 318 C; 241 G; 382 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 1288;
 Best Local Similarity 99.9%; Pred. No. 2.4e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCAGCACTAGACTATTAGCAAAATGCTTGTGATTTCCCGATATGACAGCTGCT 60
 DB 18 ATGAATGAGCAGCACTAGACTATTAGCAAAATGCTTGTGATTTCCCGATATGACAGCTGCT 77
 QY 61 TTTGGAATTTGACGTGATGAAAAACATCCACATCAAGATGACATACCTCCCTGTTATTAT 120
 DB 78 TTTGGAATTTGACGTGATGAAAAACATCCACATCAAGATGACATACCTCCCTGTTATTAT 137
 QY 121 GGCAATTATCTCTGCTGGGATTTCCAGCAATGCAATGATATCCACTTACATTTTC 180
 DB 138 GGCAATTATCTCTGCTGGGATTTCCAGCAATGCAATGATATCCACTTACATTTTC 197
 QY 181 AAAATGAGCAGCTTGAAGAGCAGCAGCAATCATTTATGCTGACCTGCGACAGATCTG 240
 DB 198 AAAATGAGCAGCTTGAAGAGCAGCAGCAATCATTTATGCTGACCTGCGACAGATCTG 257
 QY 241 CTGATCTGACAGCCTCCCTCTCTGATTTCACTACTATGATGAGGCGAAAACTGATC 300
 DB 258 CTGATCTGACAGCCTCCCTCTCTGATTTCACTACTATGATGAGGCGAAAACTGATC 317
 QY 301 TTTGAGATTTTATGATGATTTTATCCGCTCAGCTTCCATTTTCACTGATATGACAGC 360
 DB 318 TTTGAGATTTTATGATGATTTTATCCGCTCAGCTTCCATTTTCACTGATATGACAGC 377
 QY 361 ATCTCTTCTCAGCTGTTTCAAGCATCTTCCGCTACTGATGATCATTACCAATGAGC 420
 DB 378 ATCTCTTCTCAGCTGTTTCAAGCATCTTCCGCTACTGATGATCATTACCAATGAGC 437
 QY 421 TGCCTTTCCATTCACAAAACTGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 438 TGCCTTTCCATTCACAAAACTGATGATGATGATGATGATGATGATGATGATGATGAT 497
 Y 481 TCAAGTGTGCTGATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 498 TCAAGTGTGCTGATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
 QY 541 TCAAGTGTGCTGATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 558 TCAAGTGTGCTGATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 617
 QY 601 ATTTTGAAGTCACTTCTTCTGCTCCCTTGGTGAATGATGATGATGATGATGATGATGAT 660
 DB 618 ATTTTGAAGTCACTTCTTCTGCTCCCTTGGTGAATGATGATGATGATGATGATGATGAT 677
 QY 661 ATTATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 678 ATTATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
 QY 721 AGGCTAACCAATCTCTACTCTTCAATTTTATGATGATGATGATGATGATGATGATGATGAT 780
 DB 738 AGGCTAACCAATCTCTACTCTTCAATTTTATGATGATGATGATGATGATGATGATGATGAT 797
 QY 781 AGGCTAACCAATCTCTACTCTTCAATTTTATGATGATGATGATGATGATGATGATGATGAT 840
 DB 798 AGGCTAACCAATCTCTACTCTTCAATTTTATGATGATGATGATGATGATGATGATGATGAT 857
 QY 841 CATGAAGTCAATGCTTTCTAGACATTTAGTGTCTTAACACCTTTGTAACCTGTTA 900
 DB 858 CATGAAGTCAATGCTTTCTAGACATTTAGTGTCTTAACACCTTTGTAACCTGTTA 917
 QY 901 CATATGTTGTGTGATGAGCAAACTTTCAGAGGCTGTCTCAACACTGATGATGATGATGAT 960

DB 918 CTATATGTGTGTGATGAGCAAACTTTGACAGAGCTGTCTGCTCAACAGATGATGATGAT 977
 QY 961 GTAGCGGGAGCTTGTAGCAAGCAAAATTTAGTTACTCAACAGACCTTGA 1014
 DB 978 GTAGCGGGAGCTTGTAGCAAGCAAAATTTAGTTACTCAACAGACCTTGA 1031

RESULT 9
 ABL56198
 ID ABL56198 standard; DNA; 5435 BP.

XX ABL56198;
 AC 05-JUL-2002 (first entry)
 XX

DE Human P2Y1-11 encoding genomic sequence.

XX Human; P2Y1-11; chromosome 13; G protein-coupled; receptor;

KW gene therapy; thyroid; ds.

XX Homo sapiens.

OS Key Location/Qualifiers

FT CDS 318..4201 /tag- a

FT /product- "P2Y1-like purine receptor"

XX DEL0046970-A1.

XX 11-APR-2002.

PF 22-SEP-2000; 2000DE-1046970.

XX 22-SEP-2000; 2000DE-1046970.

XX (BRUE/) BRUESS M.

XX (BOEN/) BOENISCH H.

XX Bruess M, Boenisch H;

XX MPI; 2002-353329/39.

XX P-PSDB; ABB79438.

PT New human P2Y11 gene, useful for treatment and diagnosis of associated

XX disease, and related proteins, antibodies and modulators, encodes G

XX protein-coupled receptor

XX Claim 1: Page 4-5; 5pp; German.

CC The invention relates to the human P2Y11 gene (I), including its 5' and

CC 3 untranslated regions, located on chromosome 13 and encoding a G

CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies

CC etc., are used for diagnosis and (gene) therapy of diseases that are

CC (indirectly associated with (I) or its expression products. No diseases

CC are specified but as (I) is expressed only in thyroid tissue, (I) is

CC presumed to be involved in regulation of thyroid function. The present

XX sequence is that of the P2Y11 encoding genomic sequence.

Query Match 99.8%; Score 1012.4; DB 24; Length 5435;
 Best Local Similarity 99.9%; Pred. No. 5e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCAGCACTAGACTATTAGCAAAATGCTTGTGATTTCCCGATATGACAGCTGCT 60
 DB 3188 ATGAATGAGCAGCACTAGACTATTAGCAAAATGCTTGTGATTTCCCGATATGACAGCTGCT 3247
 QY 61 TTTGGAATTTGACGTGATGAAAAACATCCACATCAAGATGACATACCTCCCTGTTATTAT 120
 DB 3248 TTTGGAATTTGACGTGATGAAAAACATCCACATCAAGATGACATACCTCCCTGTTATTAT 3307


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Db      8309 ATGAATGAGCCACTAGACTATTAGCAAAAGCTTGTGATTTCCCGATTATGACAGTGTCT 8368
OY      61 TTTGGAATTTGACATGATGAAAAACATCCACATCAAGATGACTACTCTCTGTATTAT 120
Db      8369 TTTTGGAAAAATGACATGATGAAAAACATCCACATCAAGATGACTACTCTCTGTATTAT 8428
OY      121 GGCATTATCTCTCTGTGATTTCCAGGCAATGAGATGATATCCACTTACATTTTC 180
Db      8429 GGCATTATCTCTCTGTGATTTCCAGGCAATGAGATGATATCCACTTACATTTTC 8488
OY      181 AAAATGAGACCTTGAAGAGAGAGACACATCATTTATGCTGTAACCTGCGCTGACAGATCTG 240
Db      8489 AAAATGAGACCTTGAAGAGAGAGAGACACATCATTTATGCTGTAACCTGCGCTGACAGATCTG 8548
OY      241 CTGTATCTGACAGAGCTCCCTCTCTGTATGCTACTATGATGAGAGGCGAAAACTGGATC 300
Db      8549 CTGTATCTGACAGAGCTCCCTCTCTGTATGCTACTATGATGAGAGGCGAAAACTGGATC 8608
OY      301 TTTGAGATTTTCATGATGATGATTTATCCGCTCAGCTTCCATTTCAACCTGTATGACAGC 360
Db      8609 TTTGAGATTTTCATGATGATGATTTATCCGCTCAGCTTCCATTTCAACCTGTATGACAGC 8668
OY      361 ATCCCTCTCTCAGCTGTTTTCAGCATCTTCCGCTACTGATGATCATTCACCCCAATGAGC 420
Db      8669 ATCCCTCTCTCAGCTGTTTTCAGCATCTTCCGCTACTGATGATCATTCACCCCAATGAGC 8728
OY      421 TCGTTTTCATTCACAAAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db      8729 TCGTTTTCATTCACAAAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8788
OY      481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      8789 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8848
OY      541 TCAGCCTGTCTGACACTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db      8849 TCAGCCTGTCTGACACTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8908
OY      601 ATTTGACTGCACTACTTTCTGCTCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db      8909 ATTTGACTGCACTACTTTCTGCTCTCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 8968
OY      661 ATTATCCACACTCTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db      8969 ATTATCCACACTCTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9028
OY      721 AGGCTAACCATTTCTGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db      9029 AGGCTAACCATTTCTGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9088
OY      781 AGGCTAACCATTTCTGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db      9089 AGGCTAACCATTTCTGCTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9148
OY      841 CATGAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db      9149 CATGAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9208
OY      901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db      9209 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9268
OY      961 GTAGCGGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
Db      9269 GTAGCGGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9322

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RESULT 11
 AAS08362
 ID AAS08362 standard; CDNA; 1729 BP.
 XX
 AC AAS08362;

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XX      26-SEP-2001 (first entry)
DT      Human cDNA encoding G-protein coupled receptor, GPCR 39404.
DE      Human: G-protein coupled receptor; GPCR; 39404; Immunogen; antibody;
XX      Good pasture's syndrome; viral hepatitis; Alzheimer's disease; Lymphoma;
KW      Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
KW      systemic lupus erythematosus; actinic keratosis; myocarditis;
KW      Kawasaki syndrome; Dilgeorge syndrome; peripheral B-cell neoplasm;
KW      inflammations; teratoma; ss.
XX      Homo sapiens.
OS      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      CDS
FT      294..1307
FT      /tag= a
FT      /product= "protein 39404"
XX      MO200149847-A2.
XX      12-JUL-2001.
XX      22-DEC-2000; 2000MO-US35309.
XX      30-DEC-1999; 99US-0475790.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Glucksmann MA, White D;
XX      MPI: 2001-432880/46.
XX      P-PSDB; AAU04584.
XX      Novel isolated 26904, 38911 and 39404 polypeptides which are seven
XX      transmembrane proteins belonging to superfamily of G-protein-coupled
XX      receptors, useful for treating disorders of spleen, lung, liver, brain
XX      and kidney -
XX      Claim 2; Fig 1; 164pp; English.
XX      The sequence encodes a novel human seven transmembrane domain
XX      protein belonging to the G-protein coupled receptor (GPCR) superfamily,
XX      protein 39404. The receptor is useful in drug screening assays, to
XX      identify compounds that modulate receptor activity and/or interact with
XX      the receptor, and for producing antibodies specific for the receptor, its
XX      regions or fragments. The receptor is useful for treating/diagnosing a
XX      26904, 38911 and 39404 protein-associated disorder characterised by
XX      aberrant expression or activity of the protein, for monitoring
XX      therapeutic effect during clinical trials and other treatment, as bait
XX      proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
XX      analysis. The proteins and nucleic acids encoding them are useful for
XX      diagnosis and treatment of disorders selected from disorders of the
XX      spleen, lung such as Good pasture's syndrome, liver such as viral
XX      hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
XX      such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
XX      disease, colon such as Crohn's disease, uterus and endometrium such as
XX      endometriosis, T-cell disorders such as systemic lupus erythematosus,
XX      diseases of the skin such as actinic keratosis, disorders of the heart
XX      such as myocarditis, disorders involving blood vessels such as Kawasaki
XX      syndrome, disorders involving the thymus such as Dilgeorge syndrome,
XX      disorders involving B-cells such as peripheral B-cell neoplasms,
XX      disorders of the breast such as inflammations, and disorders involving
XX      the testis and epididymis such as teratoma. Numerous examples of
XX      each type of disorder are given in the specification.
XX      Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;
SO      Query Match 99.7%; Score 1010.8; DB 22; Length 1729;
      Best Local Similarity 99.8%; Pred. No. 8-2e-288;
      Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1 ATGAATGAGCCACTAGACTATTAGCAAAAGCTTGTGATTTCCCGATTATGACAGTGTCT 60

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Db      |||||||
294 ATGAATGAGCCACAGACTATTTAGCAAAAGCTTCTATTTCCCGATTATGAGCTGCT 353
QY      |||||||
61 TTTGGAATTTGACATGATGAAACATCCACTCAAGATGACATGACCTCCCGTATTTAT 120
Db      |||||||
354 TTTGGAATTTGACATGATGAAACATCCACTCAAGATGACATGACCTCCCGTATTTAT 413
QY      |||||||
121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACATGATATCCACTTACATTTTC 180
Db      |||||||
414 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACATGATATCCACTTACATTTTC 473
QY      |||||||
181 AAATGAGACCTTGGAGAGACAGACCATATTTATGCTGAACCTGGCGCTGACAGATCTG 240
Db      |||||||
474 AAATGAGACCTTGGAGAGACAGACCATATTTATGCTGAACCTGGCGCTGACAGATCTG 533
QY      |||||||
241 CTGTATCTGACAGACCTCCCTTCCTATTCATCTACTATGACATGACATGACATGATC 300
Db      |||||||
534 CTGTATCTGACAGACCTCCCTTCCTATTCATCTACTATGACATGACATGACATGATC 593
QY      |||||||
301 TTTGAGATTTTCATGTTAAATTTATCCGCTTACGCTTCCATTTCAACCTGTATAGAGC 360
Db      |||||||
594 TTTGAGATTTTCATGTTAAATTTATCCGCTTACGCTTCCATTTCAACCTGTATAGAGC 653
QY      |||||||
361 ATCCCTTCTCCACCTTCTTCCAGATCTTCCGCTACTGCTGATGATTCACCCATGAGC 420
Db      |||||||
654 ATCCCTTCTCCACCTTCTTCCAGATCTTCCGCTACTGCTGATGATTCACCCATGAGC 713
QY      |||||||
421 TGCCTTTCATTCACAAACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 480
Db      |||||||
714 TGCCTTTCATTCACAAACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 773
QY      |||||||
481 TCACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 540
Db      |||||||
774 TCACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 833
QY      |||||||
541 TCAGCCCTGCTGACCTGACAGTTCGATGATGATGATGATGATGATGATGATGATGAT 600
Db      |||||||
834 TCAGCCCTGCTGACCTGACAGTTCGATGATGATGATGATGATGATGATGATGATGAT 893
QY      |||||||
601 ATTTGACTGCACTACTTCTGCTGCTCCCTGCTGCTGATGATGATGATGATGATGAT 660
Db      |||||||
894 ATTTGACTGCACTACTTCTGCTGCTCCCTGCTGCTGATGATGATGATGATGATGAT 953
QY      |||||||
661 ATTATTCACACTGCTGACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 720
Db      |||||||
954 ATTATTCACACTGCTGACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1013
QY      |||||||
721 AGGCTAACCATTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      |||||||
1014 AGGCTAACCATTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
QY      |||||||
781 AGGCTAACCATTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db      |||||||
1074 AGGCTAACCATTTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1133
QY      |||||||
841 CATTGAGCTTACATGCTTTTACACATTAAGCTGCTGTAACACCTTTGTAACCTGTA 900
Db      |||||||
1134 CATTGAGCTTACATGCTTTTACACATTAAGCTGCTGTAACACCTTTGTAACCTGTA 1193
QY      |||||||
901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      |||||||
1194 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
QY      |||||||
961 GTTAAGGCGGAACCTTGGAGAGACAGCAAAAGAAATTTAGTTACTCAAAACACCTTGA 1014
Db      |||||||
1254 GTTAAGGCGGAACCTTGGAGAGACAGCAAAAGAAATTTAGTTACTCAAAACACCTTGA 1307

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RESULT 12
 ABV24026
 ID ABV24026 standard; cdna; 1729 BP.
 XX
 AC ABV24026;

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XX      |||||||
DT      16-SEP-2002 (first entry)
XX      |||||||
DE      Human prostate expression marker cdna 24017.
XX      |||||||
KW      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW      pharmacogenomic marker; gene; ss.
XX      |||||||
OS      Homo sapiens.
XX      |||||||
PN      WO200160860-A2.
XX      |||||||
PD      23-AUG-2001.
XX      |||||||
PF      20-FEB-2001; 2001WO-US05171.
XX      |||||||
PR      17-FEB-2000; 2000US-183319P.
PR      16-MAR-2000; 2000US-189862P.
PR      25-MAY-2000; 2000US-207454P.
PR      09-JUN-2000; 2000US-211314P.
PR      18-JUL-2000; 2000US-219007P.
PR      13-DEC-2000; 2000US-255281P.
XX      |||||||
PA      (MILL-) MILENNIUM PREDICTIVE MEDICINE INC.
XX      |||||||
PI      Schlegel R, Endege WO, Monahan JE;
XX      |||||||
DR      WPI; 2001-662795/76.
XX      |||||||
PT      Novel isolated nucleic acid molecule associated with cancerous state of
PT      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer
PS      Claim 1; Page 4453-4454; 11750pp; English.
XX      |||||||
CC      The invention relates to an isolated nucleic acid molecule (I) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (I) is useful for:
CC      (a) assessing whether a patient is afflicted with prostate cancer;
CC      (b) monitoring the progression of prostate cancer in a patient;
CC      (c) assessing the efficacy of a test compound to inhibit prostate
CC      cancer in a patient;
CC      (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC      in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound;
CC      (g) determining whether prostate cancer has metastasized in a patient;
CC      (h) assessing the aggressiveness or indolence of prostate cancer in a
CC      patient;
CC      (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX      |||||||
SQ      Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
XX      |||||||
Query Match      99.7%; Score 1010.8; DB 23; Length 1729;
Best Local Similarity      99.8%; Pred. No. 8.2e-288;
Matches 1012; Conservative      0; Mismatches      2; Indels      0; Gaps      0;
XX      |||||||
QY      1 ATGAATGAGCCACAGACTATTTAGCAAAAGCTTCTATTTCCCGATTATGAGCTGCT 60
Db      |||||||
294 ATGAATGAGCCACAGACTATTTAGCAAAAGCTTCTATTTCCCGATTATGAGCTGCT 353
QY      |||||||
61 TTTGGAATTTGACATGATGAAACATCCACTCAAGATGACATGACCTCCCGTATTTAT 120
Db      |||||||
354 TTTGGAATTTGACATGATGAAACATCCACTCAAGATGACATGACCTCCCGTATTTAT 413
QY      |||||||
121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACATGATATCCACTTACATTTTC 180
Db      |||||||
414 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACATGATATCCACTTACATTTTC 473
QY      |||||||
181 AAATGAGACCTTGGAGAGACAGACCATATTTATGCTGAACCTGGCGCTGACAGATCTG 240
Db      |||||||
474 AAATGAGACCTTGGAGAGACAGACCATATTTATGCTGAACCTGGCGCTGACAGATCTG 533

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QY 241 CTGATCTGACAGCCCTCCCTCTGATCTACTATGACAGGCGGAAAACTGATC 300
 DB 534 CTGATCTGACAGCCCTCCCTCTGATCTACTATGACAGGCGGAAAACTGATC 593
 QY 301 TTGAGAGATTTATGTTAGTTATCCGCTTACAGTTCCATTTCACCTGTATGACAC 360
 DB 594 TTGAGAGATTTATGTTAGTTATCCGCTTACAGTTCCATTTCACCTGTATGACAC 653
 QY 361 ATCCCTTCCTGACAGGCTTTCAGATCTCCGCTCTGATGATGATTCACCAATGAGC 420
 DB 654 ATCCCTTCCTGACAGGCTTTCAGATCTCCGCTCTGATGATGATTCACCAATGAGC 713
 QY 421 TCCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGAT 480
 DB 714 TCCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGAT 773
 QY 481 TCAGTGTAGCTGTATTCCTGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 774 TCAGTGTAGCTGTATTCCTGATGATGATGATGATGATGATGATGATGATGAT 833
 QY 541 TCAGCTGTGCTGACCTGACAGCTGATGATGATGATGATGATGATGATGATGAT 600
 DB 834 TCAGCTGTGCTGACCTGACAGCTGATGATGATGATGATGATGATGATGATGAT 893
 QY 601 ATTTGAGTGCACACTTCTTCTGCTCCCTGCTGATGATGATGATGATGATGATGAT 660
 DB 894 ATTTGAGTGCACACTTCTTCTGCTCCCTGCTGATGATGATGATGATGATGATGAT 953
 QY 661 ATTATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 954 ATTATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013
 QY 721 AGGCTAACCATCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 DB 1014 AGGCTAACCATCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1073
 QY 781 AGGCTAACCATCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 DB 1074 AGGCTAACCATCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1133
 QY 841 CATGAGCTTACATCT 900
 DB 1134 CATGAGCTTACATCT 1193
 QY 901 CTATATGT 960
 DB 1194 CTATATGT 1253
 QY 961 GTAAAGCGGAGACCTTGACAGCAAGCAAGAAATTTAGTACTCAAAACCCCTTGA 1014
 DB 1254 GTAAAGCGGAGACCTTGACAGCAAGCAAGAAATTTAGTACTCAAAACCCCTTGA 1307

RESULT 13
 ABV25767
 ID ABV25767 standard; cDNA; 1729 BP.
 XX ABV25767;
 AC
 XX 16-SEP-2002 (first entry)
 DT
 XX
 DE Human prostate expression marker cDNA 25758.
 XX
 KM Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KM Pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200106860-A2.
 XX 23-AUG-2001.
 PD
 XX 20-FEB-2001; 2001WO-US05171.
 PF

XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Schlegel R, Endege WO, Monahan JE;
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PS
 XX
 CC Claim 1; Page 5175-5176; 11750pp; English.
 CC
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 SO
 Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8-2e-286;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAATGAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 DB 294 ATGAATGAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 353
 QY 61 TTGGAATTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 DB 354 TTGGAATTTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
 QY 121 GGCATTATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 414 GGCATTATCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473
 QY 181 AAAATGAGACCTTGGAG 240
 DB 474 AAAATGAGACCTTGGAG 533
 QY 241 CTGATCTGACAGCCCTCCCTCTGATCTACTATGACAGGCGGAAAACTGATC 300
 DB 534 CTGATCTGACAGCCCTCCCTCTGATCTACTATGACAGGCGGAAAACTGATC 593
 QY 301 TTGAGAGATTTATGTTAGTTATCCGCTTACAGTTCCATTTCACCTGTATGACAC 360
 DB 594 TTGAGAGATTTATGTTAGTTATCCGCTTACAGTTCCATTTCACCTGTATGACAC 653
 QY 361 ATCCCTTCCTGACAGGCTTTCAGATCTCCGCTCTGATGATGATTCACCAATGAGC 420
 DB 654 ATCCCTTCCTGACAGGCTTTCAGATCTCCGCTCTGATGATGATTCACCAATGAGC 713
 QY 421 TCCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 714 TCCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGAT 773

QY 481 TCACGTGACCTGTCATTCGATGACCTTCTGTATCATCAACCAAGAGACCACAGA 540
 DB 774 TCACGTGACCTGTCATTCGATGACCTTCTGTATCATCAACCAAGAGACCACAGA 833
 QY 541 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATACATTAAGTGTACACCTA 600
 DB 834 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATACATTAAGTGTACACCTG 893
 QY 601 ATTTCGACCTCACTACTTCTGCTCCCTGCTGGTGTAGTACACTTTTGTATACACG 660
 DB 894 ATTTCGACCTCACTACTTCTGCTCCCTGCTGGTGTAGTACACTTTTGTATACACG 953
 QY 661 ATTATCCACACTCTGACCCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
 DB 954 ATTATCCACACTCTGACCCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1013
 QY 721 AGGCTAACCTTCTGCTACCTCTGCTACCTTGTATGATGATGATGATGATGATGATG 780
 DB 1014 AGGCTAACCTTCTGCTACCTCTGCTACCTTGTATGATGATGATGATGATGATGATG 1073
 QY 781 AGGCTAACCTTCTGCTACCTCTGCTACCTTGTATGATGATGATGATGATGATGATG 840
 DB 1074 AGGCTAACCTTCTGCTACCTCTGCTACCTTGTATGATGATGATGATGATGATGATG 1133
 Y 841 CATGACCTTACATCTGTTCTGTAGACATTAAGTGTGTGAACACCTTGTGTACCTGTTA 900
 DB 1134 CATGACCTTACATCTGTTCTGTAGACATTAAGTGTGTGAACACCTTGTGTACCTGTTA 1193
 QY 901 CTATATGCTGTGTCGACGCAACTTTCACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 960
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 QY 961 GTAAGCGGGAACCTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1014
 DB 1254 GTAAGCGGGAACCTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1307

RESULT 14
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 XX
 AC ABV29909;
 XX
 DT 16-SEP-2002 (first entry)
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 DE Human prostate expression marker cDNA 29900.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PS Claim 1; Page 6451; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SO Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAATGAGCAGCAGTATATTTAGCAAAATGCTGTATTTCCCGATTAAGCAGTGTCT 60
 DB 294 ATGAATGAGCAGCAGTATATTTAGCAAAATGCTGTATTTCCCGATTAAGCAGTGTCT 353
 QY 61 TTTCGAATATGACATGATGAAATCATCCACTCAAGATGACATGCTCCCTGTTATTTAT 120
 DB 354 TTTCGAATATGACATGATGAAATCATCCACTCAAGATGACATGCTCCCTGTTATTTAT 413
 QY 121 GGCATTTATCTTCCCTGCGGATTTTCCAGCAATGCAATGATGATGATGATGATGATG 180
 DB 414 GGCATTTATCTTCCCTGCGGATTTTCCAGCAATGCAATGATGATGATGATGATGATG 473
 QY 181 AAATGAGACCTTGGAGAGCAGCAGCATCTATATGCTGAACCTGGCTGCAGCATCTG 240
 DB 474 AAATGAGACCTTGGAGAGCAGCAGCATCTATATGCTGAACCTGGCTGCAGCATCTG 533
 QY 241 CTGTATCTGACACAGCTCCCTCTGATTCATCTACTATGCGCATGCGCAAAATGATG 300
 DB 534 CTGTATCTGACACAGCTCCCTCTGATTCATCTACTATGCGCATGCGCAAAATGATG 593
 QY 301 TTTCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 DB 594 TTTCGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 653
 QY 361 ATTCCTTCCGACCTGTTTCAGCATCTCCGCTGCTGATGATGATGATGATGATGATG 420
 DB 654 ATTCCTTCCGACCTGTTTCAGCATCTCCGCTGCTGATGATGATGATGATGATGATG 713
 QY 421 TGCCTTTTCATTCACAAATCGATGATGATGATGATGATGATGATGATGATGATGATG 480
 DB 714 TGCCTTTTCATTCACAAATCGATGATGATGATGATGATGATGATGATGATGATGATG 773
 QY 481 TCACGTGATGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATG 540
 DB 774 TCACGTGATGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATG 833
 QY 541 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATACATTAAGTGTACACCTG 600
 DB 834 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATACATTAAGTGTACACCTG 893
 QY 601 ATTTCGACCTCACTACTTCTGCTCCCTGCTGGTGTAGTACACTTTTGTATACACG 660
 DB 894 ATTTCGACCTCACTACTTCTGCTCCCTGCTGGTGTAGTACACTTTTGTATACACG 953
 QY 661 ATTATCCACACTCTGACCCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720

Db 954 ATTATCCACACTCTGACCATGAGACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGCA 1013
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 Db 1014 AGGCTAACCATCTCTGACTCTCTGATTTTACGATTTTATTTTACCCTCCATCTTG 1073
 QY 781 AGGCTAACCATCTCTGACTCTCTGATTTTACGATTTTATTTTACCCTCCATCTTG 840
 Db 1074 AGGCTAACCATCTCTGACTCTCTGATTTTACGATTTTATTTTACCCTCCATCTTG 1133
 QY 841 CATGAAGCTTACATCTCTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACCTGTA 900
 Db 1134 CATGAAGCTTACATCTCTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACCTGTA 1193
 QY 901 CATATATGTGTGCTGACGACCACTTTCAGCAGGCTGCTGCTCAACAGTGAATGCAAA 960
 Db 1194 CATATATGTGTGCTGACGACCACTTTCAGCAGGCTGCTGCTCAACAGTGAATGCAAA 1253
 QY 961 GTAGCGGAGACCTTGAGCAGCAAGAAATTAAGTTACTCAACAACTTGA 1014
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 XX
 AC ABV30024;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 30015.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX
 PN MO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 6487-6488; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
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 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other:
 Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 ATGATGAGCAGCACTAGACATTTAGCAAAATCTTGATTTCCCGATTAAGCAGCTGT 60
 Db 294 ATGATGAGCAGCACTAGACATTTAGCAAAATCTTGATTTCCCGATTAAGCAGCTGT 353
 QY 61 TTTGGAATTTGACATGATGAAACATCCCATCAAGATGACATACCTCCCTGTTATTTAT 120
 Db 354 TTTGGAATTTGACATGATGAAACATCCCATCAAGATGACATACCTCCCTGTTATTTAT 413
 QY 121 GGCATTATCTCTCTGCGGATTTCCAGGAAATGACATGATGATATTCATTTTC 180
 Db 414 GGCATTATCTCTCTGCGGATTTCCAGGAAATGACATGATGATATTCATTTTC 473
 QY 181 AAATGAGACCTTGAAGAGCAGCAGCAGCATCATATATCTGAACCTGGCTGACAGATCTG 240
 Db 474 AAATGAGACCTTGAAGAGCAGCAGCAGCATCATATATCTGAACCTGGCTGACAGATCTG 533
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 Db 534 CTGTATCTGACAGCCTCCCTCTGATTTCACTACTATAGCCAGTGGCGAAATCTGAT 593
 QY 301 TTTGGAATTTGACATGATGAAACATCCCATCAAGATGACATACCTCCCTGTTATTTAT 360
 Db 594 TTTGGAATTTGACATGATGAAACATCCCATCAAGATGACATACCTCCCTGTTATTTAT 653
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 Db 654 ATCCCTCCCTGACATGATGAAACATCCCATCAAGATGACATACCTCCCTGTTATTTAT 713
 QY 421 TGCCTTTCCATTCACAAACATCGATGAGTGTGAGCTGTGCTGTGATGATCATT 480
 Db 714 TGCCTTTCCATTCACAAACATCGATGAGTGTGAGCTGTGCTGTGATGATCATT 773
 QY 481 TCACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 774 TCACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
 QY 541 TCACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 834 TCACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893
 QY 601 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 894 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953
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 Db 954 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1013
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 Db 1014 AGGCTAACCATCTCTGACTCTCTGATTTTACGATTTTATTTTACCCTCCATCTTG 1073
 QY 781 AGGCTAACCATCTCTGACTCTCTGATTTTACGATTTTATTTTACCCTCCATCTTG 840
 Db 1074 AGGCTAACCATCTCTGACTCTCTGATTTTACGATTTTATTTTACCCTCCATCTTG 1133
 QY 841 CATGAAGCTTACATCTCTTCTAGACCATTAAGCTGCTCTGAAACCTTTGGTAACCTGTA 900
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Search completed: May 29, 2003, 22:24:06
Job time : 306 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 23:45:11 ; Search time 199 Seconds

(without alignments)
2283.412 Million cell updates/sec

Title: US-10-023-775B-2

Perfect score: 1771

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Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

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Database : Published.Applications_NA:

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Pred. No. is the number of results predicted by chance to have a
score greater than, or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
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2	1771	100.0	1014	US-10-270-144-1
3	1771	100.0	1014	US-10-188-405-7
4	1771	100.0	1014	US-09-885-453-2

5	1771	100.0	1014	US-09-943-798-3	Sequence 3, Appl1
6	1771	100.0	1020	US-10-270-144-3	Sequence 3, Appl1
7	1724	97.3	1020	US-09-782-974C-85	Sequence 85, Appl1
8	1444	81.5	831	US-09-943-798-1	Sequence 1, Appl1
9	1279.5	72.2	1313	US-09-728-422-1	Sequence 1, Appl1
10	940	53.1	578	US-09-782-974C-59	Sequence 59, Appl1
11	915	51.7	526	US-09-812-102-10	Sequence 40, Appl1
12	514	29.0	1429	US-09-071-173A-1	Sequence 1, Appl1
13	488	27.6	1428	US-10-270-587-1	Sequence 1, Appl1
14	487.5	27.5	993	US-09-826-791-1	Sequence 1, Appl1
15	487.5	27.5	1041	US-09-828-478-1	Sequence 1, Appl1
16	487.5	27.5	1041	US-09-826-791-5	Sequence 5, Appl1
17	487.5	27.5	1041	US-09-866-230-6	Sequence 6, Appl1
18	487.5	27.5	1260	US-09-779-679-1	Sequence 1, Appl1
19	487.5	27.5	1260	US-09-779-679-24	Sequence 24, Appl1
20	487.5	27.5	1430	US-09-828-478-3	Sequence 3, Appl1
21	487.5	27.5	1700	US-09-728-952-26	Sequence 26, Appl1
22	426	24.1	1543	US-09-891-138A-1	Sequence 1, Appl1
23	397	22.4	2577	US-09-966-755-1	Sequence 1, Appl1
24	397	22.4	2577	US-09-903-377-1	Sequence 1, Appl1
25	397	22.4	2577	US-09-952-385-1	Sequence 1, Appl1
26	397	22.4	2577	US-10-000-759A-1	Sequence 1, Appl1
27	394.5	22.3	1020	US-09-788-133-1	Sequence 1, Appl1
28	388.5	21.9	3299	US-10-208-408-24	Sequence 24, Appl1
29	379.5	21.4	1017	US-09-885-453-3	Sequence 3, Appl1
30	375.5	21.2	1080	US-09-739-151-1	Sequence 1, Appl1
31	375.5	21.2	1425	US-10-094-417-9	Sequence 9, Appl1
32	375.5	21.2	2137	US-09-782-974C-75	Sequence 75, Appl1
33	371	20.9	1065	US-09-922-895-2	Sequence 2, Appl1
34	371	20.9	1717	US-09-964-824A-100	Sequence 100, Appl1
35	371	20.9	1915	US-10-106-623-3	Sequence 3, Appl1
36	371	20.9	3426	US-10-001-835-29	Sequence 29, Appl1
37	370.5	20.9	1955	US-10-190-459-2	Sequence 2, Appl1
38	370	20.9	1689	US-09-931-381A-15	Sequence 15, Appl1
39	354	20.0	1670	US-09-880-107-2143	Sequence 2143, Appl1
40	354	20.0	1737	US-09-104-063-3	Sequence 3, Appl1
41	353.5	20.0	1068	US-10-237-563-45	Sequence 45, Appl1
42	351	19.8	1358	US-10-167-192-4	Sequence 4, Appl1
43	348	19.6	1102	US-09-870-759-143	Sequence 143, Appl1
44	348	19.6	2693	US-09-850-948-1	Sequence 1, Appl1
45	347	19.6	1014	US-09-850-948-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-10-023-775B-1
; Sequence 1, Application US/10023775B
; Publication No. US20030022282A1
GENERAL INFORMATION:
APPLICANT: Pfizer Ltd. (EP/GB only)
APPLICANT: Pfizer Inc. (US, JP, EB except GB)
APPLICANT: Fidock, Mark David
TITLE OF INVENTION: No. US20030022282A1 Polypeptide
FILE REFERENCE: PC10959A GPR
CURRENT APPLICATION NUMBER: US/10/023.775B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: GB 0030854.4
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/260,590
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: US 60/296,660
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: GB 0111031.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-775B-1

Alignment Scores:

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Score:	1771.00	Matches:	337
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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Db 421 TGCTTTTCATTCACAAACCTCATGATGCGATGTGTGAGCTGCTGGTGATGATCAT 480
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Db 481 TCACGTGATGCTGATTCGATGACCTTCCTGATCATCAACCAACAGAGCAACAGAGA 540
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
   |||||
Db 541 TCAGCTGTCTGACCTCACACCTCGGATGGAATCAATATTAATGATGATCAACCTA 600
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
   |||||
Db 601 ATTTGATGACGACACTTCTTCTGCTCCCTGCTGATGATGACACTTCTCTATACACG 660
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
   |||||
Db 661 ATATATCACACTGTGACCCATGACATGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 720
QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
   |||||
Db 721 AGGCTATACCATTTCTGACTCTTGGATTTTACGATGATTTTATTTTACCTTCAATCTTG 780
QY 261 ArgValIleArgIleLeuSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
   |||||
Db 781 AGGCTATTCGATTCGAATCTCGCTGCTTCAATCAAGTTTCCATGGAATCAGATC 840
QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleLeuAsnThrPheGlyAsnLeuLeu 300
   |||||
Db 841 CATGAGACTTACATCTTCTAGACCATTTAGCTGCTGAAACACTTTGTAACCTGTTA 900
QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
   |||||
Db 901 CTATATGTGTGTGTGACGACCAACTTTCACAGAGCTGTCTGCTCAACAGTGAATGCAAA 960

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QY 321 ValSerGlyAsnLeuGlnAlaLysIleSerTyrSerAsnAspPro 337
   |||||
Db 961 GTAGAGGGGACCTTACGACAGCAAGAAATAGTACTCAACAAACCT 1011

```

RESULT 2

US-10-270-144-1
 ; Sequence 1, Application US/10270144
 ; Publication No. US20030049790A1
 ; GENERAL INFORMATION:

APPLICANT: MET. Ming-Hui et al
 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
 ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 ; FILE OF INVENTION: PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CL000750CON
 ; CURRENT APPLICATION NUMBER: US/10/270,144
 ; PRIOR FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: 60/205,196
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-270-144-1

Alignment Scores:

Pred. No.:	1.5e-158	Length:	1014
Score:	1771.00	Matches:	337
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-023-775B-2 (1-337) x US-10-270-144-1 (1-1014)

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QY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAlaAla 20
   |||||
Db 1 ATGAATGAGACCTTACCTAATGATTTAGCAAAAGCTTGATTCCTCCCAATATGAGAGCTGCT 60
QY PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
   |||||
Db 61 TTGGAAATTTGACCTATGAAAACATCCCAATGACATGACACTCCCTGTTATTAT 120
QY GlyTleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
   |||||
Db 121 GGCATTATCTCTCCCTGGGATTTCCAGGCAATGACGATGATATCCACTTACATTTTC 180
QY LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
   |||||
Db 181 AAATATGAGACCTTGAAGAGACACCACTATATGCTGAACCTGGCTGACAGATCTG 240
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
   |||||
Db 601 ATTTGATGACGACACTTCTTCTGCTCCCTGCTGATGATGACACTTCTCTATACACG 660
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
   |||||
Db 241 CTGTATCTGACGACCTCCCTCCCTGATTCACCTACTATGCTGCGGCAAACTGGATC 300
QY 241 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
   |||||
Db 301 TTGGAGATTTGATGTTAGTTATCCGCTCAGCTTCATTTCAACCTGTATAGAGC 360
QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
   |||||
Db 361 ATCCCTCTCTCACCCTGTTTACACATCTCCGCTACTGTTGATGATCCCAAAAGAGC 420
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTrpIleIle 160
   |||||
Db 421 TGCTTTTCATTCACAAACCTCATGATGCGATGTGTGAGCTGCTGGTGATGATCAT 480
QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
   |||||
Db 481 TCACGTGATGCTGATTCGATGACCTTCCTGATCATCAACCAACAGAGCAACAGAGA 540

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QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleIleuStryrAsnLeu 200
 DB 541 TCAGGCTGCTGACCTCAGCACTGCGATGAGTGAACCTAATTAAGGGTACCACTG 600
 QY 201 IleuThrAlaThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTGACTGCAACTACTTCTTGCTCCCTGGTGAATGATGACACTTGTATACACG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlnLysAlaArg 240
 DB 661 ATTATCCACACCTGACCCCTGAGCTGCAACTGACAGCTGCTTAAGCAGAAACACGA 720
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTAACCATCTGCTACTCTTCCATTTTACGATGTGTTTACCTTCATATCTTG 780
 QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTCATTCGATCGAATCTGCTGCTTCAATCATGATGTTTCATGAGAAATCAGATC 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeu 300
 DB 841 CATGAGCTTACATGCTTCTAGACCATTAAGCTGCTGCAACACCTTGGTAACCTGTTA 900
 QY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGTGTGCTGACGAGCAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAAA 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAATTAGTACTCAACACCT 1011

RESULT 3

US-10-188-405-7
 ; Sequence 7, Application US/10188405
 ; Publication No. US20030082585A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Dai, Kang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Zhao, Jiagang
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. US20030082585A1el Receptors
 ; FILE REFERENCE: 018781-008410US
 ; CURRENT APPLICATION NUMBER: US/10/188,405
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIOR APPLICATION NUMBER: US 60/302,800
 ; FILING DATE: 2001-07-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human TGR164
 US-10-188-405-7

Alignment Scores:

Pred. No.: 1.5e-158 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775B-2 (1-337) x US-10-188-405-7 (1-1014)

QY 1 MetAsnGluProLeuAspTyrIleuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 1 ATGATGTGACCACTAGACTATTATGCAAAATGCTGTGATTTCCCGATTATGACAGCTCT 60

QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTGGAAATTCGACCTGATGAAACATCCACCTCAAGATGACACTACTCCCTTTATTTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTATCTTCCTGCTGGGATTCAGGCAATGCAAGATGATATCCACTACTATTTTC 180
 QY 61 LysMetArgProTyrIlePheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGGAAGAGCAGCAATCATATATGCAACCTGCGCTGCACAGATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTyrPhe 100
 DB 241 CTGATTCGACCAAGCTCCCTCTCTGATTCCTATGCACTGATGCAAGTGGGAAAACGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisAspAsnLeuTyrSerSer 120
 DB 301 TTGGAGATTCATGTAAGTTTATCCGCTTCACCTTCATTCACCTGATATGACAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCCCTTCCTCACCTGTTTACAGCATCTCCCTGCTGATCATTCACCAATGAGC 420
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaValTyrIleIle 160
 DB 421 TGCCTTTTCATTCACAAAATCGATGATGACGTGATGCTGTGCTGTGATGATCATT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCAGTGTAGCTGATTCCTCCGATGACCTTCCTGATCAGATCAACCAACAGGACCAAGCA 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleIleuStryrAsnLeu 200
 DB 541 TCAGGCTGCTGACCTCAGCACTGCGATGAGTGAACCTAATTAAGGGTACCACTG 600
 QY 201 IleuThrAlaThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTGACTGCAACTACTTCTTGCTCCCTGGTGAATGATGACACTTGTATACACG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlnLysAlaArg 240
 DB 661 ATTATCCACACCTGACCCCTGAGCTGCAACTGACAGCTGCTTAAGCAGAAACACGA 720
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTAACCATCTGCTACTCTTCCATTTTACGATGTGTTTACCTTCATATCTTG 780
 QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTCATTCGATCGAATCTGCTGCTTCAATCATGATGTTTCATGAGAAATCAGATC 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeu 300
 DB 841 CATGAGCTTACATGCTTCTAGACCATTAAGCTGCTGCAACACCTTGGTAACCTGTTA 900
 QY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGTGTGCTGACGAGCAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAAA 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAATTAGTACTCAACACCT 1011

RESULT 4

US-09-885-453-2
 ; Sequence 2, Application US/09885453
 ; Publication No. US20030088080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Communt, Didier
 ; TITLE OF INVENTION: RECEPTOR GPCRxi10
 ; FILE REFERENCE: 9409/2082
 ; CURRENT APPLICATION NUMBER: US/09/885,453

; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: US 09/885,453
 ; PRIOR FILING DATE: 2001-06-21
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DNA nucleotide sequence
 ; LOCATION: (1)..(1014)
 ; OTHER INFORMATION: GPCR10 DNA sequence
 ; US-09-885-453-2

Alignment Scores:

Pred. No.:	1,5e-158	Length:	1014
Score:	1771.00	Matches:	337
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-023-775b-2 (1-337) x US-09-885-453-2 (1-1014)

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QY      1 Metasngluproleuasptrylleualaasnaleseraspheproasptrylaalaala 20
DB      1 ATGAATGAGCAGCTAGCTATTAGCAAAATGCTTGATTTCCCGCATTTATGACGCTGCT 60
QY      21 Pheglvasncysrhspgluasnlleproleuysmethistyrleuprovallietyr 40
DB      61 TTTGGAAATTCAGCTGATGAAACATCCACTCAAGATGCACTCCCTGTTATTTAT 120
QY      41 Glyllelepheleuvalglypheproglyasnaalavalalleserthryrilephe 60
DB      121 GGCATTAATCTTCTCGTGGGATTTCCAGCAATGCACTAGTATTCACATTTTC 180
QY      61 Lysmetargprotrpilserserthrielleleleuansleualacystrhaspleu 80
DB      181 AAATGAGACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGCGCTGACAGATCTG 240
QY      81 Leutyrleuhrsleuropheleullehistyrrytralserserlygluasntprile 100
DB      241 CTGATCTGACACCTCCCTCCCTGATTCACATCATTCAGTGGCGAAACCTGATC 300
QY      101 Pheglvaspmetcyslysphelleargpheserphelshpheasleuetyrser 120
DB      301 TTGGAGATTTCATGTTAGTATTCGCTTCAGCTTCATTTCAACCTGTATAGCAGC 360
QY      121 IleleupheleuhrsypheSerlelephargtyrcysvalillelehisprometSer 140
DB      361 ATCCCTTCTCCTACCTGTTCCAGATCTCCGCTACTGCTGATCATTTCAACCAATGAGC 420
QY      141 Cyspheserllehislystrhargcysalavalalacyssalavalatprille 160
DB      421 TGGCTTTTCCATTCACAAACCTCGATGAGTGTATACCTGCTGCTGGGTGATATT 480
QY      161 Serleuvalalavalileprometthrpheleullehrserthrasanargthrasarg 180
DB      481 TCACGTGACCTGCTCATTCGATGACCTTCTGATCATTCACCAACAGACCAACAGA 540
QY      181 Serleuvalalavalileprometthrpheleullehrserthrasanargthrasarg 200
DB      541 TCAGCCGTCTGACACCTGACAGTGCAGATGAGTGAATCAATATTAAGTGTACAACTG 600
QY      201 IleleuhrsleuhrsypheSerleuropheleullehistyrrytralserser 220
DB      601 ATTTGAGCTGACACTACTTCTGCTCCCTGCTGATGATGACACTTCTGATACACAG 660
QY      221 Ilelehisrhleuhrsleuhrsleuvalleuvalleuvalleuvalleuvalleuval 240
DB      661 ATTAATCCACACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
  
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QY      241 Argleuhrsleuhrsleuvalleuvalleuvalleuvalleuvalleuvalleuval 260
DB      721 AGGCTAACCTATCTGCTACCTCTGATTTAGTATGTTTATACCTTCATATCTTG 780
QY      261 Argvalillearglleuhrsleuvalleuvalleuvalleuvalleuvalleuval 280
DB      781 AGGCTAACCTATCTGCTACCTCTGATTTAGTATGTTTATACCTTCATATCTTG 840
QY      281 Hisglualatryllevalserargproleualaaleuansnthrpheglvasleu 300
DB      841 CATGAGCTTACATCTGCTTCTAGACCATTAATGCTGCTGACACCTTGTGATCTGTA 900
QY      301 Leutyrvalavaliseraspasphinglinalavalacyserthryalargcyslys 320
DB      901 CTATATGCTGCTGCTGACGACCACTTACGACGAGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY      321 Valserglysnleuuglinalalylslyllestrtyserasnspro 337
DB      961 GTAAGGGGGAACCTTGAGCAAGCAAGAAATTAATGATCAAAACCTT 1011
  
```

RESULT 5

US-09-943-798-3

; Sequence 3, Application US/09943798
 ; Patent No. US20020065215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glaxo Group Limited
 ; TITLE OF INVENTION: Polypeptide
 ; FILE REFERENCE: 061021
 ; CURRENT APPLICATION NUMBER: US/09/943,798
 ; FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-943-798-3

Alignment Scores:

Pred. No.:	1,5e-158	Length:	1014
Score:	1771.00	Matches:	337
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-023-775b-2 (1-337) x US-09-943-798-3 (1-1014)

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QY      1 Metasngluproleuasptrylleualaasnaleseraspheproasptrylaalaala 20
DB      1 ATGAATGAGCAGCTAGCTATTAGCAAAATGCTTGATTTCCCGCATTTATGACGCTGCT 60
QY      21 Pheglvasncysrhspgluasnlleproleuysmethistyrleuprovallietyr 40
DB      61 TTTGGAAATTCAGCTGATGAAACATCCACTCAAGATGCACTCCCTGTTATTTAT 120
QY      41 Glyllelepheleuvalglypheproglyasnaalavalalleserthryrilephe 60
DB      121 GGCATTAATCTTCTCGTGGGATTTCCAGCAATGCACTAGTATTCACATTTTC 180
QY      61 Lysmetargprotrpilserserthrielleleleuansleualacystrhaspleu 80
DB      181 AAATGAGACCTTGGAAAGACAGACCATCATTAATGCTGAACCTGCGCTGACAGATCTG 240
QY      81 Leutyrleuhrsleuropheleullehistyrrytralserserlygluasntprile 100
DB      241 CTGATCTGACACCTCCCTCCCTGATTCACATTCAGTGCAGTGGCGAAACCTGATC 300
QY      101 Pheglvaspmetcyslysphelleargpheserphelshpheasleuetyrser 120
DB      301 TTGGAGATTTCATGTTAGTATTCGCTTCAGCTTCATTTCAACCTGTATAGCAGC 360
QY      121 IleleupheleuhrsypheSerlelephargtyrcysvalillelehisprometSer 140
  
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|||||
Db 361 AACCTTCCTCACCCTGTTGACGACATCTCCGCTACTGCTGATCATTCACCAATGAGC 420
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaAlaCysAlaValAlaIle 160
Db 421 TGCCTTTTCATTCACAAAACCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 161 SerLeuValAlaValAlaIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 481 TCACGTGACGTGCTGATTCCTGATCCATCTTCTGATCATCATCAACCAAGGACCAACAGA 540
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
Db 541 TCAGCCTGCTCGACCTGACAGCTGCGATGATGATCAATCAATATTAAGTGAACACCG 600
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db 601 ATTTTGACCTGCAACACTTTCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
Db 661 ATTATCCACACTCTACCCATGAGTGCACAACTGACAGCTGCCCTTAAGCAGAAAGACAGA 720
QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheThrValCysPheLeuProPheHisIleLeu 260
Db 721 AGGCTAACCATCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db 781 AGGGTCATTCGGATGGAATCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 281 HisGluAlaThrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeu 300
Db 841 CATGAAGCTTACATGCTTCTGACCATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 301 LeuThrValAlaValSerAspAsnPheGlnAlaValCysSerThrValArgCysLys 320
Db 901 CTATATGTGTGTGTGCTGACGACCAACTTTCAGCAGGCTGCTGCTCAACAGTGAATGACAA 960
QY 321 ValSerGlyAsnLeuGlnAlaValLysLysIleSerTyrSerAsnAsnPro 337
Db 961 GTAAAGGGGAACCTTGAGCAAGCAAAAGAAATTAAGTACTCAAAACACCT 1011

RESULT 6
US-10-270-144-3
; Sequence 3, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CLO00750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9905
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-3

Alignment Scores:
Pred. No.: 4,07e-157 Length: 9905
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-10-023-775b-2 (1-337) x US-10-270-144-3 (1-9905)
QY 1 MetAsnGluProLeuAspTyrIleuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
Db 8309 ATGAATGAGCACCTAGACATTAATTAAGCAATGCTTGAATTTCCCGCATTAATCAGCTGCT 8368
QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
Db 8369 TTGGAAATGACATGATCAAAAACATCCACATCAAGATCATCTACTCCCTGTTATTTAT 8428
QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValAlaIleSerThrTyrIlePhe 60
Db 8429 GGCATTATCTCTCGTGGGATTCAGGCAATGAGTAGATATCCACTTACATTTTC 8488
QY 61 LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
Db 8489 AAAATGAGACCTTGGAAAGAGCAGCACATCAATTAAGCTGAACCTGCGCCGACAGATTCG 8548
QY 81 LeuThrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTrpIle 100
Db 8549 CTGTATCTGACAGCCCTCCCTCTCTGATTCCTACTATGCCAGTGGGCAAAACCTGATC 8608
QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuThrSer 120
Db 8609 TTGGAGATTTTCATGTGTGAATTAACGCTTACACTTCCATTTCAACCTGATATGACAGC 8668
QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisThrMetSer 140
Db 8669 ATCCCTTCCCTCACCCTGTTTCAGATCTTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8728
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaAlaCysAlaValAlaIle 160
Db 8729 TGCCTTTTCATTCACAAAACCTGATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 8788
QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 8789 TCACGTGAGAGCTGTGATTCGATCCGATGACCTTGTGATCAATCAACCAAGCAGCAACAGA 8848
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
Db 8849 TCAGCCTGCTCTGACCTCAACGCTGCGATGAGCAATCAATTAAGTGAAGGACCAACCTG 8908
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db 8909 ATTTGACCTGCAACACTTTCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8968
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
Db 8969 ATTATCCACACTCTGACCATGAGTGCACAACTGACAGCTGCCCTTAAGCAGAAACAGAGA 9028
QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheThrValCysPheLeuProPheHisIleLeu 260
Db 9029 AGGCTAACCATCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9088
QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db 9089 AGGCTCATTCGGATGGAATCTGCTGCTCTTCAATCAAGTGTTCATTGACATGACATGATC 9148
QY 281 HisGluAlaThrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeu 300
Db 9149 CATGAAGCTTACATGCTTCTGACCATTAAGCTGCTGACACACTTGGTGAACCTGTATA 9208
QY 301 LeuThrValAlaValSerAspAsnPheGlnAlaValCysSerThrValArgCysLys 320
Db 9209 CTATATGTGTGTGTGCTGACGACCAACTTTCAGCAGGCTGCTGCTCAACAGTGAATGACAA 9268
QY 321 ValSerGlyAsnLeuGlnAlaValLysLysIleSerTyrSerAsnAsnPro 337
Db 9269 GTAAAGGGGAACCTTGAGCAAGCAAAAGAAATTAAGTACTCAAAACACCT 9319

RESULT 7
US-09-782-974C-85
; Sequence 85, Application US/09782974C

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Publication No. US20030082534A1
GENERAL INFORMATION:
APPLICANT: Vogel, Gabriel
APPLICANT: Lind, Peter
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
FILE REFERENCE: 41USPHM311
CURRENT APPLICATION NUMBER: US/09/782,974C
PRIOR FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/714,449
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 1020
ORGANISM: Homo sapiens
US-09-782-974C-85

Alignment Scores:
Pred. No.: 4 27e-154 Length: 1020
Score: 1724.00 Matches: 335
Percent Similarity: 99.12% Conservative: 2
Best Local Similarity: 98.53% Mismatches: 0
Query Match: 97.35% Indels: 3
DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-782-974C-85 (1-1020)
QY 1 Metasngluproleuasptryleualasnalaseraspheproasptryalaala 20
DB 4 ATGAATGAGGACCTAGACATTTAGCAAAATGCTTGATTTCCCGCATTTAGCAGCGCT 63
QY 21 PhcglYAsncysThrspguasnllleproleuylskethistyrleuprovallle 40
DB 64 TTTGGAATGTGACCTGTGAAAACATCCCACTCAAGATGACCACTCCCTGTTATTTAT 123
QY 41 GlyllellepheleuvalglypheproglyAsnalavalallieserthrtyrlephe 60
DB 124 GGCATATATCTTCTCGTGGGATTTCCAGGCAATGCAATGATATATCATTTTTC 183
QY 61 LysmetlarpProtrpyllysserSerthllellewelleuasnleualacysthAspleu 80
DB 184 AAATAGAGACCTTGGAAAGACACACATCATATGCTGAACCTGGCTGCACAGATCTG 243
QY 81 LeutyrleuthrserleupropheleuillhistyrtyrAlaserglyluasntpille 100
DB 244 CTGTATCTGACCGCCCTCCCTCCGATTCACATCATCTCCAGTGCGAAACTGGATC 303
QY 101 PhcglYAspthehetcylyspheilleargPheSerperhehisphasleuLeutyrSer 120
DB 304 TTTGGAGATTTCATGtGTAAgTTATCCGCTTCAGCTTCATTCATTCACCTGTATAGCAGC 363
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QY 121 lleleupheleuthrcyspheserllepheargtyrcysvalillellehsPrometSer 140
DB 364 ATCCTTCTCTACCGTGTTCAGACATCTCCGCTACTGTGTATCATTCACCAATAGAG 423
QY 141 CyspheserllehisysthrarGysalavalalCysalavalaltrpillelle 160
DB 424 TGCTTTTCATTCACAAACTCGATGTCAGTGTGAGCTGTCCTGTGTGTGATCAT 483
QY 161 SerleuValalavalillepometthrphleuilllethSerthrasnargthrasnarg 180
DB 484 TCACGTGAGCTGTCAATCCGATGACCTCTTGTATCATCAACCAAGACCAACAGA 543
QY 181 SerAlaCysleuaspheuthrSerSerAspgluLeuasnThrilleysttryAsnleu 200
DB 544 TCAGCGTGTCTGACCTGACCACTGGATGGAAGCTCAATCATTTAAGTGATGACACCTG 603
QY 201 lleleuthrAlathrThrphcysleuproleuvalillevalthreucysytrthrthr 220
DB 604 ATTTGACTGCAAGTACTTCTGCTCCCTCCCTGGTATGATGACACTTGTCTATACACG 663
QY 221 llellehsThrleuthrHlsglyleuGlnThrAspSerCysleuysglnysAlaArg 240
DB 664 ATATTCACACTTTGACCCATGAGCTGCAGAAAGCTGACCTTAAAGCAAGAACACGA 723
QY 241 ArgleuthrilleleuLeuLeuAlapheryValCysphleuProphehisilleu 260
DB 724 AGGCTAACCATCTGCTACTCTTGCAATTTAGATGTTTATACCTTCATATCTTG 783
QY 261 Argvalille-Argillegluserarg-LeuuserlleserCysserllegluasngln 280
DB 784 AGGCTAATTCAGATGAAATCTCAGCTGCTTCAATCACTTTCATTCAGAAATCAGA 843
QY 280 lehsGluAlatyrillevaliserArgProleu-AlaAlaleuasnThrphcglYAsnleu 299
DB 844 TCCATGAGCTTACATCTGTTCTAGACCATATGCTGCTGTGAACCTTGGTAACCTG 963
QY 300 LeuleuthrValavalalSerAspasnphcglnglnalavalCysserthrValArgys 319
DB 904 TTACTATATGTGTGTGTCAGCAGCAACTTTCACAGAGCTGTGCTCAACAGAGATGTC 963
QY 320 LysvaliserlYasnleuGlnAlalylsilleserYrserAsnAspPro 337
DB 964 AAAGTAAGCGGGAACCTTGAGCAAGCAAAATAATTAATTCACCAACACCTC 1017

RESULT 8
US-09-943-798-1
; Sequence 1, Application US/09943798
; Patent No. US20020065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: 061021
; CURRENT APPLICATION NUMBER: US/09/943,798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-943-798-1

Alignment Scores:
Pred. No.: 1 03e-127 Length: 831
Score: 1444.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 81.54% Indels: 0
DB: 10 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-943-798-1 (1-831)
QY 62 MetlarpProtrpyllysserSerthllellewelleuasnleualacysthAspleu 81
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Db 1205 ATATTCACACTGTCACCATGAGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGA 1264
Qy 241 ArgLeuThrIleLeuLeu 247
Db 1265 AGGCTAACCAATCTGCTACTC 1285

RESULT 10
US-09-782-974C-59/C
: Sequence 59, Application US/09782974C
: Publication No. US20030082534A1
: GENERAL INFORMATION:
: APPLICANT: Vogel, Gabriel
: APPLICANT: Lind, Peter
: APPLICANT: Wood, Linda S.
: APPLICANT: Parodi, Luis A.
: TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
: FILE REFERENCE: 41USPHRM311
: CURRENT APPLICATION NUMBER: US/09/782,974C
: CURRENT FILING DATE: 2002-09-04
: PRIOR APPLICATION NUMBER: 60/165,838
: PRIOR FILING DATE: 1999-11-16
: PRIOR APPLICATION NUMBER: 09/714,449
: PRIOR FILING DATE: 2000-11-16
: PRIOR APPLICATION NUMBER: 60/198,568
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: 60/166,071
: PRIOR FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 60/166,678
: PRIOR FILING DATE: 1999-11-19
: PRIOR APPLICATION NUMBER: 60/173,396
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: 60/184,129
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: 60/185,421
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: 60/185,554
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: 60/186,530
: PRIOR FILING DATE: 2000-03-02
: Remaining Prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 192
: SOFTWARE: Patent version 3.1
: SEQ ID NO 59
: LENGTH: 578
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-782-974C-59

Alignment Scores:
Pred. No.: 3.2e-80 Length: 578
Score: 940.00 Matches: 189
Percent Similarity: 98.45% Conservative: 2
Best Local Similarity: 97.42% Mismatches: 0
Query Match: 53.08% Indels: 3
DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-782-974C-59 (1-578)
Qy 130 PheArgTyrCysValIleIleHisPrometSerCysPheSerIleHisLysThrArgCys 149
Db 577 TTCGGCTACGTGTGATCATTCACCAATGAGCTGCTTTCATTCACAAATCGATGT 518
Qy 150 AlaValAlaCysAlaValAlaValTrpIleIleSerLeuValAlaValIlePrometThr 169
Db 517 GCAGTTAGCGCTGTGCTGTGATCATTTCACTGTGAGCTGTGATTCATTCGATGACC 458
Qy 170 PheLeuIleThrSerThrAsnArgThrAsnArgSerAlaCysLeuAspLeuThrSerSer 189
Db 457 TTCCTGATCAGATCAACCAAGACAGACAGATGAGCTGTGACCTGACCAAGTTGC 398
Qy 190 AspGluLeuAsnThrIleLysTrpTyrAsnLeuLeuThrAlaThrThrPheCysLeu 209
Db 397 GATGAACTCAATACTATTAAAGTGTACAACTGATTTGACTGCAAGTACTTCTGCTC 338

Qy 210 ProLeuValIleValIleThrLeuCysTyrThrIleIleHisThrLeuThrHisGlyLeu 229
Db 337 CCCTGGATAGTACAGACTTGTCTATACAGAGTATTCACACTTTGACCAAGGACTG 278
Qy 230 GluThrAspSerCysLeuLysGlnLysAlaArgArgLeuThrIleLeuLeuLeuAla 249
Db 277 CAAGTACAGCTGCTTAAAGCAAGAAAGCAGAGGCTAACCAATTCGTACTCTTGGCA 218
Qy 250 PheTyrAlaCysPheLeuProPheHisIleLeuArgValIle-ArgIleGlySerArg-L 269
Db 217 TTTCAGTATGTTTTCACCTTCATATCTTGAGGGCTCATTCGAGATCGAATCTCAGCC 158
Qy 269 euleuSerIleSerCysSerIleGluAsnGlnIleHisGluAlaTyrIleValSerArgp 289
Db 157 TGCTTCAATCAGTGTTCATTCAGATGAGATCCATGAAAGCTTACATGCTTCTAGAC 98
Qy 289 roleu-AlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrValAlaValSerAspAsn 308
Db 97 CATATGCTGCTCGAACACCTTTGGTAACTGTACTATATGTGTGTGACGACAC 38
Qy 309 PheGlnGlnAlaValCysSerThrValArgCysLys 320
Db 37 TTCAGCAGGCTGTCTGCTCAACAGTAGATGACAA 2

RESULT 11
US-09-812-102-40/C
: Sequence 40, Application US/09812102
: Patent No. US20020055179A1
: GENERAL INFORMATION:
: APPLICANT: Robison, Keith E
: TITLE OF INVENTION: No. US20020055179A1 G-Protein Coupled Receptor Homologs
: FILE REFERENCE: 5800-41 035800/183478
: CURRENT APPLICATION NUMBER: US/09/812,102
: CURRENT FILING DATE: 2001-03-19
: PRIOR APPLICATION NUMBER: Prior
: PRIOR FILING DATE: 1999-07-30
: NUMBER OF SEQ ID NOS: 90
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 40
: LENGTH: 526
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: GPCR-RHODOPSIN
US-09-812-102-40

Alignment Scores:
Pred. No.: 6.5e-78 Length: 526
Score: 915.00 Matches: 171
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 51.67% Indels: 0
DB: 10 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-812-102-40 (1-526)
Qy 87 ProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTrpIlePheGlyAspPheMetCys 106
Db 526 CCCTTCCTGATTCATCTATGACAGTGGCAGAAAGTGAATCTTTGAGATTTGATGTGT 467
Qy 107 LysPheIleArgPheSerPheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCys 126
Db 466 AAGTTATCGCTTCACCTTCACCTGATGAGCAATCCCTTCCTGACCTGT 407
Qy 127 PheSerIlePheArgTyrCysValIleHisPrometSerCysPheSerIleHisLys 146
Db 406 TTCAGCATCTCCCTGCTGTGATCATTCACCAATGAGCTGCTTTCATTCACAAA 347
Qy 147 ThrArgCysAlaValAlaCysAlaValAlaValTrpIleIleSerLeuValAlaValIle 166
Db 346 ACTGAGTGTGAGTGTGAGCTGTGCTGTGTGTGTGATCATTTTCAGTGTGATCATTT 287

Alignment Scores:

Pred. No.: 7.42e-37 Length: 1428
 Score: 488.00 Matches: 111
 Percent Similarity: 56.21% Conservative: 61
 Best Local Similarity: 36.27% Mismatches: 122
 Query Match: 27.56% Indels: 12
 DB: 9 Gaps: 6

US-10-023-775b-2 (1-337) x US-10-270-587-1 (1-1428)

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QY 23 AsnGysThrAspGluAsn-----IleProLeuLysMetHisTyrLeuPro 37
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 AATGCAACTGCCAAATGCTGCGACGACGAGGCTCCCGGAAAGTACTACTTCC 172
QY 38 ValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThr 57
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 ATTTTATGAGATGAGATGCTGTTGGAGTCTTGGAATATACATGTTGTTAGGCG 232
QY 58 TyrIlePheLysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCys 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 TACATCTCTCTGAGAGAACTGGACAGCATATATATCTTAACTTACTCTCTC 292
QY 78 ThrAspLeuTyrIleThrSerIleHisTyrArgCysAlaValAlaCysAlaVal 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 293 TCTGACTTACTTCTTCTGTCACCTCCCATGCTGTATAGAGATTATGCCAATGGA 349
QY 98 AsnTrrIlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeu 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 350 AACTGATATATGAGAGAGCTGCTGCATAGCAACCGAATATGCTTCATGCCAACCTC 409
QY 118 TyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgGlyTyrCysValIleIleHis 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 TATACCGACATCTCTTCTTCTCATTATGACATATATGATCTGATATATATAGTAT 469
QY 138 PrometSerCysPheSerIleHisTyrArgCysAlaValAlaCysAlaVal 157
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 CTTTCCGAGAACACCTTCTGCAAAAGAGAGTGTCTATTTAATCTCCCTGGCCATG 529
QY 158 TrrIleLeuSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArg 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 TGGGTTTATGATACCTTATGAGATTTACTACCATCTCCCTTAAATTCGTATATACT 589
QY 178 ThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrr 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 GACAAATGGCACACCTGATTAATGATTTGCAAGTTCTGAGAGCCCACTCAACCTCAT 649
QY 198 TyrAsnLeuLeuThrAlaThrThrPheCysLeuProLeuValIleAlaThrLeuCys 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 650 TACAGCATGTGTCTAACACAGCTGGGTTCTTCTTCTTTTGTGATGTGTTTCTT 709
QY 218 TyrThrThrIle--IleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLys 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 710 TATTTACAAATGCTCTCTCTTAACAGAGAGAAATGAGAGGTTGCTACTGCTGCC 769
QY 237 ---GlnLysAlaArgAlaGlyLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeu 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 770 CTTGAAAGGCTCTCAACTTGGTGCATGATGCAATGCTTCTCTGCTTGTTCACA 829
QY 256 ProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer-----Ile 272
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 830 CCTTATACGTCATGCGGAATGTGAGGATGCTTACGCGCTGGGAGATTGGAACTAT 889
QY 273 SerCysSerIleGluAsnGlnIleHisGluAlaTyrIleValSerArgProLeuAlaAla 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 890 CAGTGGACT---CAGGTCGTCACTCACTCTTTTACTTGTGACAGGCGCTGTGCTTT 946
QY 293 LeuAsnThrPheGlyAsnLeuLeuTyrValAlaValSerAspAsnPheGlnAlaAla 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 947 CTGACAGGTGTCACTCACTCTCTTCTTATTTCTTGTGGAGATCACTTACAGGACATG 1006
QY 313 ValCysSerThrValArg 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1007 CTGATGATCACTCACTGAGA 1024
  
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RESULT 14

US-09-826-791-1

Sequence 1, Application US/09826791

Patent No. US20010039037A1

GENERAL INFORMATION:

APPLICANT: Pfizer Inc

TITLE OF INVENTION: No. US20010039037A1el Polypeptide

FILE REFERENCE: PC10914ADAM

CURRENT APPLICATION NUMBER: US/09/826,791

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 0008504.3

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: 60/198,367

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 993

TYPE: DNA

ORGANISM: Homo sapiens

US-09-826-791-1

Alignment Scores:

Pred. No.: 4.89e-37 Length: 993
 Score: 487.50 Matches: 111
 Percent Similarity: 55.03% Conservative: 64
 Best Local Similarity: 34.91% Mismatches: 114
 Query Match: 27.53% Indels: 29
 DB: 10 Gaps: 10

US-10-023-775b-2 (1-337) x US-09-826-791-1 (1-993)

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QY 23 AsnGysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyrGlyIle 42
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 AACTGCAATTTGAAAC-----TTCAAGAGAAATTTTCCCAATTTGATATGATA 93
QY 43 IlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePheLysMet 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 ATATTTTCTGGGAGAGCTTGGAAATGCG-----TTGTCATATATGTTTTC--CTG 144
QY 63 ArgProTrrPlySerSerThr-----IleIleMetLeuAsnLeuAlaCysThrAsp 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 CAGCTTATTAAGAGATGACATGTCGATGACGTTTCTGCTAATGCTAAATGCGCATTT 204
QY 80 LeuLeuTyrLeuThrSerLeuProPheLeuIleHisTyrTrrAlaSerGlyLysAsnTrr 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 CTCTGTTCATTAAGACGCTTCCCTTACAGGCTGACTATATATCTTACAGGCTCCAA 264
QY 100 IlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 ATATTGAGACACCTGGCCTGACAGATTAATGCTTATATCTTGTATGCAACATGTA 324
QY 120 SerIleLeuPheLeuThrCysPheSerIlePheArgGlyTyrCysValIleIleHisPromet 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 AGTATTTATTTCTGACCGCTGCTGAGTGTGTGCTTCTGCAATAGGTTCAACCTTT 384
QY 140 SerCysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTrrPile 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 CGGCTTGCATGTCACACAGATCAGAGAGTCCGATCTCTGTGGATCATATGATC 444
QY 160 IleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsn 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 CTATATCATGCTTCCCTCAATA-----ATGCTCTGACAGATGCTCTGAGACAGAC 495
QY 180 ArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys----- 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 GCGAGT-----GTCACTATCATGCTTATAGAGTGTGATCTTATTAATATGCTAAG 543
QY 197 -----TrrTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleVal 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 CTGACAGCATGATATATATGCTTGTGTGGCTGCTGCTGCTGCTTTCACACATC 603
  
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OY 215 ThrleuCystrThrThrIleIleHisThrleuThrHisGlyLeuGlnThrAspSerCys 234
DB 604 AGCATCTGTATCTGCTGATCATCTGGGTTCTGTTAAAGTGAGAGTCCCAATTCGGGG 663
OY 235 LeuLys-----GlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
DB 664 CTGGGGTTTTCACAGAGAGGAGGAGTCCACCATCATCATCATCTGATCATCTTCTTC 723
OY 253 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer 271
DB 724 TTGTTTCTCTCCCTGATCAGACACTGAGACCGCTGCTGATGACAGCAATGAAATGGGT 783
OY 272 IleSerCysSerIleGluAsnGlnIleHisGluAlaTyrIleValSerArgProLeuAla 291
DB 784 TTA-----TGCAGAGACAGACTGCATTAAGCTTTGGTTATCATCACTGGCCTTGGCA 834
OY 292 AlaLeuAsnThrPheGlyAsnLeuLeuLeuTyrValValSerAspAsnPheGlnGln 311
DB 835 GCAGCCAAATGCTGCTCAATCATCTGCTCTATTAATTTGCTGGGAGAAATTTTAAGGAC 894
OY 312 AlaValCysSerThrValArgCysLysValSerGlyAsnLeuGlnAlaLys 329
DB 895 AGACTAAAGTCTGACTCAGA-----AAAGGCATCCACAGAGGCAAG 939

RESULT 15
US-09-828-478-1
; Sequence 1, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-828-478-1

Alignment Scores:
Pred. No.: 5,24e-37 Length: 1041
Score: 487.50 Matches: 111
Percent Similarity: 55.03% Conservative: 64
Best Local Similarity: 34.91% Mismatches: 114
Query Match: 27.53% Indels: 29
DB: 9 Gaps: 10

US-10-023-775b-2 (1-337) x US-09-828-478-1 (1-1041)
OY 23 AsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyrGlyIle 42
DB 88 AACTGCACAATTTGAAC-----TTCAAGAGAGAAATTTTCCCAATGTATATCGATA 141
OY 43 IlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePheLysMet 62
DB 142 AATATTTTCTGGGGAGTCTTGGGAAATGG-----TTGTCATATATATGTTTC--CTG 192
OY 63 ArgProTyrLysSerSerThr-----IleIleMetLeuAsnLeuAlaCysThrAsp 79
DB 193 CAGCCTTATTAAGATCCCATCTGTAAGAGTTTTCATGCTTAATCTGGCCATTTCAAGAT 252
OY 80 LeuLeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTyr 99
DB 253 CTCCTGTTTCATTAAGACAGCTCTCCCTTCAAGGAGCTGATATTAATCTTAAGAGCTCAATGG 312

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OY 100 IlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 119
DB 313 AATATTTGGAGAGACTGGCCTGCAGAGATTAATGCTTATCTTGTATGTAACATGTAAC 372
OY 120 SerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMet 139
DB 373 AGTATTTATTTCTGACCGCTGAGATGTTGAGGCTTCTGCGCAATGATGATCAACCCCTT 432
OY 140 SerCysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrIle 159
DB 433 CGGCTTCTGCATGTCACAGATCCAGATGAGTGGCTGATCTCTGTTGGATATGAGATC 492
OY 160 IleSerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsn 179
DB 493 CTATATCATGCTTCCCAAT-----ATGCTTCTGAGACAGTGGCTGAGAGCAAG 543
OY 180 ArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys----- 196
DB 544 GGCAGT-----CTCACATCATGCTTAAGAGCTGAATCTATTAATTTGCTAAG 591
OY 197 -----TPTTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleVal 214
DB 592 CTGAGACCATGAGACTATATATTCCTGTTGTTGGGCTGCTGCTGCAATTTTTCACACATC 651
OY 215 ThrleuCystrThrThrIleIleHisThrleuThrHisGlyLeuGlnThrAspSerCys 234
DB 652 AGCATCTGTATCTGCTGATCATCTGGGTTCTGTTAAAGTGAGAGTCCCAATTCGGGG 711
OY 235 LeuLys-----GlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
DB 712 CTGGGGTTTTCACAGAGAGGAGGAGTCCACCATCATCATCATCTGATCATCTTCTTC 771
OY 252 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer 271
DB 772 TTGTTTCTCTCCCTGATCAGACACTGAGACCGCTGCTGATGACAGCAATGAAATGGGT 831
OY 272 IleSerCysSerIleGluAsnGlnIleHisGluAlaTyrIleValSerArgProLeuAla 291
DB 832 TTA-----TGCAGAGACAGACTGCATTAAGCTTTGGTTATCATCACTGGCCTTGGCA 882
OY 292 AlaLeuAsnThrPheGlyAsnLeuLeuLeuTyrValValSerAspAsnPheGlnGln 311
DB 883 GCAGCCAAATGCTGCTCAATCATCTGCTCTATTAATTTGCTGGGAGAAATTTTAAGGAC 942
OY 312 AlaValCysSerThrValArgCysLysValSerGlyAsnLeuGlnAlaLys 329
DB 943 AGACTAAAGTCTGACTCAGA-----AAAGGCATCCACAGAGGCAAG 987

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Search completed: May 30, 2003, 01:16:12
 Job time : 206 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 22:24:09 ; Search time 295 Seconds
(without alignments)
2572.622 Million cell updates/sec

Title: US-10-023-775b-2
Perfect score: 1771
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239.seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1771	100.0	1011	22 AAL43942	Human G protein-co
2	1771	100.0	1014	24 AAS07948	Human cDNA encodin
3	1771	100.0	1014	24 AB078887	Human G-protein co
4	1771	100.0	1014	24 ABN85630	Human P2Y-1-like rec
5	1771	100.0	1014	24 AAD34278	Human AXOR89 (G-pr
6	1771	100.0	1014	24 ABK11381	Human DNA encoding
7	1771	100.0	1014	24 AAK98323	Human purinergic-r
8	1771	100.0	1014	24 AAD26370	Human G-protein co
9	1771	100.0	1288	24 AB156197	Human P2Y-11 enco
10	1771	100.0	5435	24 AB156198	Human P2Y-11 enco
11	1771	100.0	9905	24 AAK98324	Human purinergic-r
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13	1764	99.6	1729	23 ABY24026	Human prostrate exp
14	1764	99.6	1729	23 ABY25767	Human prostrate exp
15	1764	99.6	1729	23 ABY29909	Human prostrate exp
16	1764	99.6	1729	23 ABY30024	Human prostrate exp
17	1724	97.3	1020	22 AAH51011	Human nGPCR54 codl
18	1444	81.5	831	24 ABN85629	Human P2Y-1-like rec
19	1279.5	72.2	1313	22 AAK52430	Human polynucleotl
20	993	56.1	740	23 ABY15662	Human prostrate exp
21	940	53.1	578	22 AAK50998	Human nGPCR54 codl
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23	861.5	48.6	545	22 AAK53414	Human polynucleotl
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25	751	42.4	539	23 ABY45465	Human prostrate exp
26	623	35.2	478	23 ABY15479	Human prostrate exp
27	617	34.8	426	23 ABY36271	Human prostrate exp
28	617	34.8	426	23 ABY45310	Human prostrate exp
29	597	33.7	2245	24 ABK11380	Human P2Y-1-like G
30	595	33.6	435	23 ABY06310	Human prostrate exp
31	567	32.0	6721	24 AAS18599	Purinergic recepto
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33	550	31.1	442	23 ABY08973	Human prostrate exp
34	514	29.0	1429	18 AAT74321	Human P2Y4 recepto
35	492	27.8	1428	18 AAT75146	Human ATP recepto
36	491.5	27.8	1041	22 AAS08000	Human cDNA encodin
37	487.5	27.5	993	24 AAH77276	Human G-protein co
38	487.5	27.5	1026	24 AAS98140	Human DNA for pote
39	487.5	27.5	1039	22 AAS10778	DNA encoding cyste
40	487.5	27.5	1041	22 AAD26608	Human P2Y-1-like GPC
41	487.5	27.5	1041	22 AAS07941	Human cDNA encodin
42	487.5	27.5	1041	24 AAD28591	Human CysLT2 GPCR
43	487.5	27.5	1041	24 AAH77279	Human G-protein co
44	487.5	27.5	1260	22 AAD13709	Human G-protein co
45	487.5	27.5	1430	22 AAK26609	Human P2Y-1-like GPC

ALIGNMENTS

RESULT 1
ID AAL43942 standard; DNA: 1011 BP.
XX AAL43942:
XX

DT 27-SEP-2002 (first entry)

DE Human G protein-coupled receptor coding sequence.

XX Human; gene therapy; G protein-coupled receptor; drug development;

KW central nervous system disease; endocrine disease; metabolic disease;

KW cancer; respiratory disease; digestive disease; immune disease;

KW inflammation; infection; circulatory disease; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.

XX (AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Lowitz KP;

DR WPI: 2001-355616/37.

DR P-PSDB: AAU04375.

PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX Claim 55; Page 113-114; 159pp; English.

XX The sequence encodes a human G-protein coupled receptor (GPCR),
 CC hRUP21. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system. Incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 4.97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-10-023-775b-2 (1-337) x AAS07948 (1-1014)

OY 1 MetAngLpProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
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 DB 61 TTGGAAATTCGACGATGAAACATCCACATGAGATGCACTACTCCCTGTTATTTAT 120
 OY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTATCTCTCTGCTGGATTCAGGCAATGAGTATGATATCCACTTACATTTTC 180
 OY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGGAGAGACGACCATCATTAATGCTGAGCTGACAGATCTG 240
 OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTyrPile 100

DB 241 CTGTATCTGACAGCCTCCCTTCGATTCACACTACTACTATGACAGTGGCAAAATGATAC 300
 OY 101 PheGlyAspPheMetCysLysPheIleAlaGphSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTGGAGATTTATGATGATGATTTATCCCTTCAGCTTCATTTCAACTGATATACACAC 360
 OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
 DB 361 ATCCCTTCCTTACCTGCTTTCAGCATCTTCGCCGCTACTGTGTATCTTACCACATGAC 420
 OY 141 CysPheSerIleHisLysThrArgCysAlaValAlaIleCysAlaValAlaTyrIleIle 160
 DB 421 TCGTTTTCATTCACAAACATCGATGTGAGTTGTAGCTGTGCTGTGTGTGATCATTT 480
 OY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCAGCTGTAGCTGTCTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 540
 OY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
 DB 541 TCAGCTGTGTGACCTTCACAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 600
 OY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTGACTGCAACTGCTTTCGCTCCCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 OY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATTATCCACACTGTGACCCATGACACTGACAGCTGACAGCTGACAGCTGACAGCTGACAG 720
 OY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTACCACTTCTGCTACTCTTCGATTTTACGATTTTATTTTACCCTTCATATCTTG 780
 OY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
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 OY 281 HisGluAlaThrIleValSerArgProLeuAlaIleLeuAsnThrPheGlyAsnLeuLeu 300
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 DB 901 CTATATGCTGTGCTGACGACCAACTTTCAGCAGCGCTGTCTGCTACACATGATGATCA 960
 OY 321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
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 ID ABO78847
 ID ABO78847 standard; cDNA; 1014 BP.
 AC ABO78847;
 XX
 DT 04-OCT-2002. (first entry)
 XX
 DE Human G-protein coupled receptor PFI-019 cDNA.
 XX
 KW Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
 KW anti-inflammatory; cytoskeletal; cardiovascular; antiallergic; hypotensive;
 KW arteriosclerosis; osteoporosis; hypertension; asthma;
 KW artherosclerosis; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /tag= a
 FT /product= "PFI-019"
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 PN EP1219638-A2.

XX 03-JUL-2002.
 PD 04-DEC-2001; 2001EP-0310136.
 XX 18-DEC-2000; 2000GB-0030854.
 PR 04-MAY-2001; 2001GB-0011031.
 XX (PE12) PFIZER LTD.
 PA (PE12) PFIZER INC.
 XX FIDOCK MD;
 PI WPI: 2002-521945/56.
 DR P-PSDB: ABB81902.
 XX New G-protein coupled receptor (GPCR) polypeptide with homology to p2y
 PT putinoceptor, useful for treating e.g. inflammation or cancers in a
 PT patient, or for screening GPCR agonists or antagonists for treating
 PT these diseases
 XX Claim 1; Page 12; 19pp; English.
 PS The invention relates to a novel G-protein coupled receptor (GPCR), and
 CC the polynucleotide encoding it. The protein of the invention has
 CC neuroprotective, anti-inflammatory, cytosolic, cardiovascular,
 CC antiallergic, hypotensive, antiarteriosclerotic, and osteopathic
 CC activity. The GPCR polypeptide is useful for manufacturing a medicament
 CC for treating a patient who needs to upregulate a receptor. Preferably,
 CC therapeutically useful areas are hypertension, asthma, and
 CC atherosclerosis. The sequence encodes the G-protein coupled receptor
 CC of the invention, PFI-019.
 XX
 SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;
 Alignment Scores:
 Pred. No.: 4.97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-10-023-775b-2 (1-337) x ABQ7847 (1-1014)
 QY 1 MetasngluproleuaspTYrleuAlaasnAlaseraspPheproAspTYrAlaAla 20
 DB 1 ATGATGAGCCACTAGACTATTAGCAATGCTCTGATTTCCCGATTATGACGCTGCT 60
 QY 21 PheGlyasnCysThrAspGluasnIleProleuLysMetHisTYrleuProValIleTYr 40
 DB 61 TTGGAATTTGCACTGATGAAACATCCCACTCAAGATGACACTACCTCCCTGATTTAT 120
 QY 41 GIVTlellePheleuValIGlyPheProGlyAsnAlaValIleSerThyTYrIlePhe 60
 DB 121 GGCTTATATCTTCCGCGGGGTTTCCAGGCATACAGATGATATCCACTTACATTTTC 180
 QY 61 LysMetArgProTyrPlysSerSerThrIleIleMetLeuAsnAlaCysThrAspLeu 80
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 DB 241 CTGTATCTGACACACCTCCCTTCCTGATTCATCATATGCACTGGGGAAGAACTGATC 300
 QY 101 PheGlyaspPheMetCysPheIleArgPheSerPheHisPheAsnLeuTYrSerSer 120
 DB 301 TTGGAATTTGCACTGATGAAACATCCCACTCAAGATGACACTACCTCCCTGATTTAT 360
 QY 121 IleleuPheleuThrCysPheSerIlePheArgTYrCysValIleIleHisPheMetSer 140
 DB 361 ATCTCTTCTCTACCTGTTTTCAGCATCTTCCGCTACTGTGTGATCATTTACCAATGAGC 420

QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTYrIle 160
 DB 421 TGCTTTCCATTCACAAACGTCAGATGTCACATTTGCTGCTGGTGGATCATTT 480
 QY 161 SerLeuValAlaValIlePrometThrPheleuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCACGTGAGCTGTCATTCCTCCGATGACCTTCTTGATCATCAACCAACAGACCAAGAGA 540
 QY 181 SerAlaCysIleuAspLeuThrSerSerAspGluAsnThrIleLysTYrTYrAspLeu 200
 DB 541 TCAGCTGTCTGACCTCCACGTCGATGACACTCAATCATTAATTAAGTGTACACCTA 600
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 DB 661 ATATCCACACTCTGACCCCATGACAGCTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTYrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGCTTAACCAATTCGCTACTCTCTCTGCTTACATTTACATGATTTTACCTTCATATCTTG 780
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTATTCGATCGATGATATCGCTGCTTCATCAAGTGTTCATATGAGAAATCAGATC 840
 QY 281 HisGluAlaTYrIleValSerArgProleuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 841 CATTAACCTTACATCGTTTTCAGACATTTACTCTCTGCAACACTTGTGTAACCTTCTTA 900
 QY 301 LeuTYrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGTGTGTGCTGACGACGACACTTTCAGAGCTGTCTGCTCAACAGTGAATGCAAA 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTYrSerAsnAsnPro 337
 DB 961 GTAGCGGGGAACCTTGAGCAAGCAAAATAATGTTACTCAACCAACCCCT 1011
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 ID ABBN85630 standard; DNA; 1014 BP.
 AC ABBN85630;
 XX 18-SEP-2002 (first entry)
 DE Human P2Y₁-like receptor variant encoding gene SEQ ID NO 3.
 DE Human; P2Y₁-like receptor; HIPHUM 0000037; immunity; inflammation;
 KW cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
 KW immunomodulator; anti-inflammatory; cytosolic; antistatic;
 KW gastrointestinal; anti-ulcer; antirheumatic; antiallergic; virocidic;
 KW antibacterial; immunosuppressive; dermatological; nephrotropic;
 KW antiallergic; analgesic; receptor; gene; ds.
 XX Homo sapiens.
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 XX
 FH key Location/Qualifiers
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 FT /*tag= a
 FT /product= "P2Y₁-like receptor variant"
 PN GB2369364-A.
 XX 29-MAY-2002.
 PD 31-AUG-2001; 2001GB-0021215.
 PF 01-SEP-2000; 2000GB-0021524.
 PR 06-SEP-2000; 2000GB-0021894.
 PR 25-SEP-2000; 2000GB-0023444.

XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Foord SM, Ignar DM;
 PI
 XX WPI: 2002-511268/55.
 DR P-PSDB; ABB83819.
 XX
 PT An isolated p2y-like receptor polypeptide (HIPHM 0000037) which can be
 PT used for the identification of agonists and antagonists which may be
 PT used to treat an immune or inflammatory disease -
 XX
 XX Claim 5; Page 28-29; 35pp; English.
 CC The invention relates to an isolated p2y-like receptor polypeptide
 CC (ABB83818-ABB83819) which is also referred to in the specification as
 CC HIPHM 0000037. An effective amount of a substance (agonist or
 CC antagonist) which modulates p2y receptor activity is useful to treat a
 CC subject having a disorder that is responsive to p2y-like receptor
 CC modulation. The disorder is a disease of immunity or inflammation. The
 CC substance may also be used to manufacture a medicine for the treatment or
 CC prophylaxis of a disorder that is responsive to stimulation or modulation
 CC of p2y-like receptor activity. Disorders which may be treated include
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
 CC polymyositis or prostatitis. The invention provides alternative
 CC substances for the treatment of immunological and inflammatory diseases.
 CC The present sequence is that the p2y-like receptor variant encoding gene
 CC of the invention.
 XX
 XX SQ Sequence 1014 BP: 258 A; 263 C; 189 G; 304 T; 0 other:
 Alignment Scores:
 Pred. No.: 4,97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-10-023-775B-2 (1-337) x ABB85630 (1-1014)
 DY 1 MetasnGLUPROLeuAsPTyLeuAlaAsnAlaSerAspPheProAspTyAlaAla 20
 DB 1 ATGAATGAGCCACTGACTATTACCAATGCTTCTGATTCCCGATTATGCAGCTGCT 60
 QY 21 PheGLyAsnCysThAspGLyAsnIleProLeuLysMetHisTyLeuProValIleTyr 40
 DB 61 TTTCGAAATGTCACATGATGAAGAAACATCCACATCAAGATGACTACCTCTTATTTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGLyAsnAlaValIleSerThTyIlePhe 60
 DB 121 GGCATTATCTCTCTGCGGATTCAGAGCAATGAGATGATATCCACTTACATTTTC 180
 QY 61 LysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGGAAGACGACGACCATATTATGCTGACCTGCGACAGATCTG 240
 QY 81 LeuTyIleuThrSerLeuProPheLeuIleHisTyTyAlaSerGlyGluAsnTyrPhe 100
 DB 241 CTGATCTGACCAAGCTCTCCCTCTGATTCACATCACTATGCGAGGCGAAACATGATC 300
 QY 101 PheGLyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTTCGAGATTCATCATGTAAGTTATCCGCTTCACCTTCACATTCACCTGTATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCTCTTCTCTACACTGTTTCAGCATCTTCGCGCTACTGTGATCATTCACCAATAGAGC 420

QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaIaCysAlaValAlaTyrPheIle 160
 DB 421 TCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCACGTGTGATGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 540
 QY 181 SerAlaCysLeuAsnLeuThrSerSerAspGlyIleuAsnTyrIleLysTyrPyrAsnLeu 200
 DB 541 TCAGCTGTGCTGACCTCACAGCTTCGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyTyThrThr 220
 DB 601 ATTTTGACATGCAACTACTTTCGCTCCCTGCGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATTATCCACACTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 720
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTAACATTCCTGCTACTCTTGCATTTCATGATGATGATGATGATGATGATGATGATGAT 780
 QY 261 ArgValIleArgIleGlySerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTAACATTCCTGCTACTCTTGCATTTCATGATGATGATGATGATGATGATGATGATGAT 840
 QY 281 HisGluAlaTyrTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeu 300
 DB 841 CATGAAGCTTACATCTCTTCTGACCTTACATGATGATGATGATGATGATGATGATGATGAT 900
 QY 301 LeuTyValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAspAsnPro 337
 DB 961 GTTACGGGACACTTGTGACGACCAAGAAATATTAGTTACTCAAAACACCT 1011
 RESULT 5
 AAD34278
 ID AAD34278 standard; cDNA; 1014 BP.
 XX
 AC AAD34278;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Human AXOR89 (G-protein coupled receptor) cDNA.
 XX
 KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
 KW Infection; cancer; pain; asthma; Parkinson's disease; diabetes; obesity;
 KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;
 KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
 KW myocardial infarction; allergy; benign prostatic hyper trophy; migraine;
 KW vomiting; psychotic; neurological disorder; anxiety; manic depression;
 KW delirium; Huntington's disease; Gilles de la Tourette's syndrome;
 KW dementia; dyskinesia; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /tag= a
 FT /product= "Human AXOR89 protein"
 XX
 PD GB2365012-A.
 XX
 PN 13-FEB-2002.
 XX
 PF 10-MAY-2001; 2001GB-0011437.
 XX
 PR 11-MAY-2000; 2000US-0569137.

XX 14-AUG-2000: 2000US-224989P.
 PR (FARB) BAYER AG.
 PA
 XX Ramakrishnan S;
 PI
 DR MPI; 2002-257607/30.
 DR P-PSDB; AAU77600.
 XX

PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can
 be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 XX

PS Claim 1: Fig 5; 118pp; English.

XX The invention relates to a purified human P2Y1-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y1-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence encodes the P2Y1-like GPCR of the invention.
 XX

SO Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 4.97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775B-2 (1-337) x ABK1381 (1-1014)

QY 1 MetaAngluProleuAspTyrleuAlaAnaIAserAspPheProAspTyrAlaAla 20
 DB 1 AAGAAATGAGCCACTGACTATTTAGCAAAATGCTTGCATTTCCCATTAACAGCTGCT 60
 QY 21 PheGlyAsnGlyThrAspGluAsnIleProleuLysMetHisTyrleuProValIleTyr 40
 DB 61 TTGGAAATGTCACATGATATAAACAATCCACATCAAGATCAGTACTCTCTGTATTAT 120
 QY 41 GlyIleIlePheleuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTAATCTCTCGTGGGATTTCCAGCAATGCGATGATATCCACTACATTTTC 180
 QY 61 LysMetArgProTyrIleSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAAGAGACCTTGGAAAGACGACCAATCATTAATGCTGACCTGCGACAGATCTG 240
 QY 81 LeuTyrleuThrSerleuProPheleuIleHisTyrTyrAlaSerGlyGluAsnTyrPle 100
 DB 241 CTGTATCTGACACGCTCCCTTCTGATTCACATCTATGCGAGGCGAAACATGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisIleAsnLeuTyrSerSer 120

DB 301 TTGGAGATTTCACTGTGTAAGTTTATCCGCTTCAGCTTCATTTCAACCTGATATACAGC 360
 QY 121 IleleuPheleuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCCTCTCTCCACCTGCTTTCAGCAATCTTCGCTACCTGTGTATCATCAACCAATGAGC 420
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaValAlaCysAlaValAlaTyrPleIle 160
 DB 421 TGCTTTTCATTTACAAACATCGATGCGAGTGTGACCTGTGCTGTGTGTGATCAT 480
 QY 161 SerleuValAlaValIleProMetThrPheleuIleHisSerThrAsnArgThrAsnArg 180
 DB 481 TCACCTGTGAGCTGTCAATTCGATGACCTTCTTGATATCAATCAACCAACAGACACAGA 540
 QY 181 SerIleCysLeuAsnIleuThrSerSerAspGluLeuAsnThrIleLysTyrAsnLeu 200
 DB 541 TCAGCCTGTCTCAGCTTCACCAACATTCGAGTGAAGTCAATATCTATTAAGTGTACACCTG 600
 QY 201 IleleuThrAlaThrThrPheCysLeuProleuValIleValThrIleuCysTyrThrThr 220
 DB 601 ATTTTACCTGACACCTACTTTCTGCTCCCTTGCTGTATGATGACACTTGTCTATACACG 660
 QY 221 IleIleHisThrleuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATATCCACACTCTGACCCATGAGCTGCAAACTGACAGCTGCTTAAGCAGAAAGACAGA 720
 QY 241 ArgleuThrIleleuLeuLeuAlaPheTyrValCysPheleuProPheHisIleleu 260
 DB 721 AGGCTTACCACTTCTGCTACCTTGCATTTTATGATATGTTTATACCTTCCATATCTTG 780
 QY 261 ArgValIleArgIleGlnSerArgleuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTATTCGATTCGATTCGATTCGCTGCTTTCATATCATGTTTCCATTTGAGATTCGATC 840
 QY 281 HisGluAlaTyrIleValSerArgProleuAlaAlaLeuAsnThrPheGlyAsnLeu 300
 DB 841 CATGAAGCTTACATCTGCTTCTAGACCATTAAGTCTGTGAACACCTTGTGTATACCTGTTA 900
 QY 301 LeuTyrValAlaValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGTGTGTGTGACGCGCAACTTTCAGCAGCTGTCTGCTCAACAGATGATCCAA 960
 QY 321 ValSerGlyAsnLeuGlnAlaValLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAGCGGAGACCTTGACGACGAAAGAAATTAATGTTACTCAAAACACCT 1011

RESULT 7
 ID AAK98323 standard; cDNA; 1014 BP.
 NC AAK98323;
 XX
 DT 30-APR-2002 (first entry)
 XX
 DE Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.
 KW Human; chromosome 13; purinergic GPCR: G-protein coupled receptor;
 KW signal transduction; human protease; GPCR disorder; gene therapy;
 KW transgenic animal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1014
 FT CDS /tag- a
 PF /product- "G-protein coupled receptor"
 PN MO200187980-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US15957.
 XX

/product- "Human GCRBC-2 protein"

FT XX MO200187937-A2.
 PN XX 22-NOV-2001.
 PD XX 17-MAY-2001; 2001WO-US16285.
 PF XX 18-MAY-2000; 2000US-205628P.
 PR XX 22-MAY-2000; 2000US-206222P.
 PR XX 25-MAY-2000; 2000US-207566P.
 PR XX 02-JUN-2000; 2000US-208834P.
 PR XX 02-JUN-2000; 2000US-208861P.
 PA (INCYTE GENOMICS INC.)
 PI Paterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R;
 PI Khan FA, Gandhi AR, Walla NK, Nguyen DB, Yue H, Hatalia A;
 PI Elliott VS, Lai P, Reddy R, Kalliock DA, Tang TY, Au-Young J;
 XX MPI: 2002-089844/12.
 DR P-PSDB; AAE16171.
 XX
 PT Novel G-protein coupled receptors and polynucleotides useful for
 PT diagnosis, treatment and prevention of disorders of cell proliferation,
 PT neurological, cardiovascular, metabolic disorders and viral infections
 PT
 XX
 PS Claim 5; Page 111-112; 115pp; English.
 XX
 CC The invention relates to human G-protein coupled receptor (GCRBC)
 CC polypeptides and polynucleotides. GCRBC polypeptides are useful for
 CC screening compounds that modulate their activity. They are useful in
 CC the diagnosis, prevention and treatment of disorders which include
 CC cell proliferative disorders such as arteriosclerosis, hepatitis,
 CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukemia,
 CC lymphoma; neurological disorders such as epilepsy, ischemic
 CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
 CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
 CC meningitis, Creutzfeldt-Jacob disease, schizophrenia disorders, amnesia;
 CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
 CC hypertension, vascular tumors, myocardial infarction, hypertensive
 CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;
 CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,
 CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
 CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
 CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
 CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
 CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
 CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
 CC fungal, parasitic, protozoal and helminthic infections and trauma;
 CC metabolic disorders such as diabetes, obesity and osteoporosis; and
 CC viral infections such as infection caused by viral agent classified as
 CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention
 CC are useful as probes for assessing toxicity of test compounds. They are
 CC also used in gene therapy. The present sequence is human G-protein
 CC coupled receptor 2 (GCRBC-2) cDNA.
 CC
 XX
 SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 4,97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775b-2 (1-337) x AAD26370 (1-1014)

OY I MetasnglProLeuAspPtyrLeuAlaAsnAlaSerAspPheProAspPtyrAlaAla 20
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db	1	ATGAATGAGCAGCACTAGATATTAGCAAAATGCTCTGATTTCCCGATTATGACCTGCT	60
OY	21	PheGlyAsnGlyThrAspGluAsnIleProLeuGlyMetHisTyrLeuProValIleTyr	40
Db	61	TTTGGAAATGACATGATGAAAAACATCCACATCAAGATGACCTGCTCTGATTTAT	120
OY	41	GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe	60
Db	121	GGCATTATCTCTCTGCTGGGATTTCCAGCAATGCAATGATGATATCCATTACATTTTC	180
OY	61	LysMetArgProTyrPlysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu	80
Db	181	AAATGAGACCTTGGAAAGAGCAGCACATCATATTATGCTGAGCTGCGCTGCACAGATCTG	240
OY	81	LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnProPle	100
Db	241	CTGTATCTGACCGAGCTCCCTCTCTGATTCATCTCATGCGCAAGGGCAAAACGTGATC	300
OY	101	PheGlyAspPheMetCysLysPheIleArgPheSerPheHisAsnLeuTyrSerSer	120
Db	301	TTTGGAGATTTCATGTGTAAGTTTATCCGCTTCACCTTCATTACCTGTAATGACAC	360
OY	121	IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer	140
Db	361	ATCCCTTCCTCCACCTGTTTCAGATCTTCCCTACTGCTGATGATTCACCCAAATGAGC	420
OY	141	CysPheSerIleHisIleGlyThrArgCysAlaValAlaIleCysAlaValAlaIlePle	160
Db	421	TGCTTTTCCATTCACAAAACCTGATGTCAGTTGATGCTGCTGCTGCTGCTGCTGCTGCT	480
OY	161	SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg	180
Db	481	TCACGTGATGAGCTGATTCATTCGATGATCTTTCATGATCAATCAACAGAGCAACAGA	540
OY	181	SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu	200
Db	541	TCAGCTCTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT	600
OY	201	IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr	220
Db	601	ATTGTTGACGTGCAACACTGCTTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
OY	221	IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlyGlnIleAsnArg	240
Db	661	ATTATCCACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT	720
OY	241	ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu	260
Db	721	AGGCTAACCAATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	780
OY	261	ArgValIleArgIleGlySerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle	280
Db	781	AGGCTCATTCGAGTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	840
OY	281	HisGluAlaTyrIleValSerArgProLeuAlaIleAsnThrPheGlyAsnLeuLeu	300
Db	841	CATGAGCTTACATGCTTTCATGACCATTTAGCTGCTGCAACACCTTTGCTGCTGCTGCTGCT	900
OY	301	LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys	320
Db	901	CTATATGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	960
OY	321	ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro	337
Db	961	GTAACGGGGAACCTTGAGCAAGCAAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT	1011

RESULT 9
 ABL56197 standard; cDNA; 1288 BP.
 XX ABL56197;
 AC
 XX
 DT 05-JUL-2002 (first entry)

XX	DE	Human P2Y1-1i encoding cDNA.
XX	KW	Human; P2Y1-1i; chromosome 13; G protein-coupled; receptor;
XX	KW	gene therapy; thyroid; gene; ss.
XX	OS	Homo sapiens.
XX	PH	Key
XX	ET	Location/Qualifiers
XX	ET	CDS
XX	XX	18..1031
XX	XX	/tag="a
XX	XX	/product="P2Y1-like purine receptor"
XX	XX	DE10046970-A1.
XX	XX	11-APR-2002.
XX	XX	22-SEP-2000; 2000DE-1046970.
XX	XX	22-SEP-2000; 2000DE-1046970.
XX	PA	(BRUE/) BRUESS M.
XX	PA	(BOEN/) BOENISCH H.
XX	XX	Bruess M, Boenisch H;
XX	XX	WPT; 2002-353329/39.
XX	DR	P-PSDB; ABB79438.
XX	PT	New human P2Y1i gene, useful for treatment and diagnosis of associated
XX	PT	diseases, and related proteins, antibodies and modulators, encodes G
XX	PT	protein-coupled receptor
XX	PS	Claim 5; Page 3; 5pp; German.
XX	XX	The invention relates to the human P2Y1i gene (I), including its 5' and
XX	CC	3' untranslated regions, located on chromosome 13 and encoding a G
XX	CC	protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies
XX	CC	etc., are used for diagnosis and (gene) therapy of diseases that are
XX	CC	(in)directly associated with (I) or its expression products. No diseases
XX	CC	are specified but as (I) is expressed only in thyroid tissue, (I) is
XX	CC	presumed to be involved in regulation of thyroid function. The present
XX	CC	sequence is that of the P2Y1i encoding cDNA.
XX	XX	Sequence 1288 BP; 347 A; 318 C; 241 G; 382 T; 0 other;
XX	XX	Alignment Scores:
XX	XX	Pred. No.: 6,68e-145 Length: 1288
XX	XX	Score: 1771.00 Matches: 337
XX	XX	Percent Similarity: 100.00% Conservative: 0
XX	XX	Best Local Similarity: 100.00% Mismatches: 0
XX	XX	Query Match: 100.00% Indels: 0
XX	XX	DB: 24 Gaps: 0
XX	XX	XX-10-023-775B-2 (1-337) x ABL56197 (1-1288)
XX	XX	1 MetAsnGluPProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAlaAla 20
XX	XX	18 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGATTTCCCGATTATGACGCTGCT 77
XX	XX	21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
XX	XX	78 TTTGGAAATTTGACGTCATGAAACATCCACATCAAGATGACATACCCCTGTTATTAT 137
XX	XX	41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValValIleSerThrTyrIlePhe 60
XX	XX	138 GGCATTATCTTCCTGCTGGGATTTCCAGCAATGCGAGTATGATTCACATTTCATTTTC 197
XX	XX	61 LysMetArgProTyrIlePheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
XX	XX	198 AAAATGAGACCTTGGAGAGCAGCAGCACCATCATTTATGCTGAACCTGGCGCTCACAGATCTG 257
XX	XX	81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyAsnTyrPle 100

Db	258	CTGTACTGTACGACGCTCCCTCCCTGATCTACTACTATGCGACATGGGGAAACTGGATC	31.7
Oy	101	PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer	120
Db	318	TTTGGAGATTTCATGTGTAAAGTTTATCCGCTTCACGCTTCACCTTTCACCTGTATAGCAGC	37.7
Oy	121	IleIleuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPromSer	14.0
Db	378	ATCCTCTCTCCACCGTTCAGACATCTTCGCTACTGTGTGATCATTCACCCATAGC	43.7
Oy	141	CysPheSerIleHisTyrThrArgCysAlaValAlaIaCysAlaValAlaTyrPleIle	16.0
Db	438	TGCTTTTCCATTACAAAACCTGGATGTGACGTGTAGCCTGTGCTGTGTGATATAT	49.7
Oy	161	SerIleuValAlaValIlePromethrPheLeuIleThrSerThrAsnArgThrAsnArg	18.0
Db	498	TCACCTGGTACGTGTCAATTCGGATGACCTTCCTGATCACAATCAACCAAGACCAACAGA	55.7
Oy	181	SerAlaCysLeuAspLeuThrSerSerAspGluAsnThrIleLysTTPTrpTyrAsnLeu	20.0
Db	558	TCAGCCGTCTCCACCTCCACCGATTCGGATGAACTCAATTAATTAAGTGTACAACTCG	61.7
Oy	201	IleIleuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr	22.0
Db	618	ATTTTGACGTCAACATCTATTCTTGCCCTCCCTGGTGATGAGACATTTGCTATACACG	67.7
Oy	221	IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg	24.0
Db	678	ATTATCCACACTCTGACCCATGGACTGGCAAACTGACACTGCTCTTAAGCAAAAGCAGCA	73.7
Oy	241	ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu	26.0
Db	738	AGGCTTAACCTTTCTGCTACTCTCTGATTTTACGTATCTTTTAAACCTTCACATCTTG	79.7
Oy	261	ArgValIleIleArgIleLeuSerArgPheLeuSerIleSerCysSerIleGluAsnGlnIle	28.0
Db	798	AGGCTATTCGTGGATCGAATCTGCGCTTCCTCAATCAAGTGTCTTCATTTGAGAAATCAGATC	85.7
Oy	281	HisGluAlaTyrIleValSerArgProLeuAlaIleAsnThrPheGlyAsnLeuLeu	30.0
Db	858	CATGAAGCTTACACTCTCTCTGACCATTAAGCTGCTGGAACACTTTGGTAACCTGTTA	91.7
Oy	301	LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys	32.0
Db	918	CTATTAGTGTGGTGCAGCACAACCTTTCAGCAGCGCTGTCTCAACAGTGTGATGCCAA	97.7
Oy	321	ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro	33.7
Db	978	GTAAGCGGGAACTTGTAGCAACAAAGAAATTAATTACTCAACAACACCT	102.8
RESULT 10			
ABL56198	standard; DNA; 5435 BP.		
XX	ABL56198;		
AC	05-JUL-2002 (first entry)		
XX			
DT			
XX	Human P2Y1-1i encoding genomic sequence.		
DE			
XX			
XX	Human; P2Y1-1i; chromosome 13; G protein-coupled; receptor;		
KW	gene therapy; thyroid; ds.		
RW			
XX			
XX	Homo sapiens.		
XX			
EH	Key	Location/Qualifiers	
FT	CDS	318..4201	
FT		/*tag= a	
FT		/product= "P2y1-Like purine receptor"	
XX			
FN	DE10046970-AL.		

PD 11-APR-2002.
 XX 22-SEP-2000; 2000DE-1046970.
 PF 22-SEP-2000; 2000DE-1046970.
 XX
 PR 22-SEP-2000; 2000DE-1046970.
 XX
 XX (BRUE/) BRUESS M.
 PA (BOEN/) BOENISCH H.
 XX
 PI Bruess M, Boenisch H;
 XX
 DR WPI; 2002-353329/39.
 DR P-PSDB; ABB79438.
 XX
 PT New human P2Y11i gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 PS
 XX Claim 1; Page 4-5; 5pp; German.

CC The invention relates to the human P2Y11i gene (I), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies
 CC etc., are used for diagnosis and (gene) therapy of diseases that are
 CC (in)directly associated with (I) or its expression products. No diseases
 CC are specified but as (I) is expressed only in thyroid tissue, (I) is
 CC presumed to be involved in regulation of thyroid function. The present
 CC sequence is that of the P2Y11i encoding genomic sequence.

XX Sequence 5435 BP; 1509 A; 1168 C; 996 G; 1762 T; 0 other;

Alignment Scores:

Pred. No.: 3,986-144 Length: 5435
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775B-2 (1-337) * ABL56198 (1-5435)

OY 1 MetasnguIProleuAspTYrLeuAlaAsnAlaSerAspPheProAspTYrAlaAla 20
 DB 3188 ATGAATGAGCCACTGATCTATTAGCAATGCTTGTGATTCGCCGATTATGACACTGCT 3247
 OY 21 PheGlyAsnCySThAspGluAsnIleProLeuLysMetHisTYrLeuProValIleTYr 40
 DB 3248 TTGGAAATTGACATGATGAAGAAACATCCACATCAAGATGACACTCCCTGTTATTTAT 3307
 OY 41 GlyIleIlePheLeuValIGlyPheProGlyAsnAlaValIleSerThrTYrIlePhe 60
 DB 3308 GGCATTATCTCTCTGCTGGATTTCCAGGCAATGCAATGATATTCACCTTACATTTTC 3367
 OY 61 LysMetArgProTyrPheSerSerThrIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 3368 AAAATGAGACCTTGAAGAGGAGCAGCATCATTAATGCGAAGCTGCGCCGACAGATGCG 3427
 OY 81 LeuTYrLeuThrSerLeuProPheLeuIleHisTYrTYrAlaSerGlyGluAsnTrpIle 100
 DB 3428 CTGTATCTGACACGCTCCCTCTCTGATTCACACTACTATGCGAGGCGAAACAGATC 3487
 OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTYrSerSer 120
 DB 3488 TTGGAGATTTCATGTTGTAAGTTTATCGCTTCACCTTCACCTTCAACCTGTATGACAGC 3547
 OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTYrCysValIleIleHisProMetSer 140
 DB 3548 ATCCCTTCCTCCTACCTGTTTCAGCATCTTCGCTCTCTGTCATCATTCACCAATGAGC 3607
 OY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTrpIleIle 160
 DB 3608 TGCCTTTCATTCACAAACAACTGATGTCAGTTGAGCTGTGCTGTGTGATCATCTT 3667

OY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThraAsnArg 180
 DB 3668 TCACGTGCTGCTGCTATTCATTCGATGACCTCTTGATCAGCATCAACCAAGAGCAACAGA 3727
 OY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTYrAsnLeu 200
 DB 3728 TCAGCTGCTGCTGACCTCAGCTCAGCTTGCATGAGTCAATCAATCAATCAATCAATCA 3787
 OY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTYrThrThr 220
 DB 3788 ATTTGACTGCAACTACTTCTGCTCCCTCCCTGGATGATGATGATGATGATGATGATGATG 3847
 OY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 3848 ATTATCCACACTCTGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3907
 OY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTYrValCysPheLeuProPheHisIleLeu 260
 DB 3908 AGGCTAACCATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3967
 OY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 3968 AGGGTCATTCGGATGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4027
 OY 281 HisGluAlaTYrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 4028 CATGAAGCTTACATGCTTCTTGACCATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4087
 OY 301 LeuTYrValAlaValSerAspAsnPheGlnAlaAlaValCysSerThrValArgCysLys 320
 DB 4088 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4147
 OY 321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTYrSerAsnAsnPro 337
 DB 4148 GTAAAGCGGAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCT 4198
 RESULT 11
 AAK98324
 ID AAK98324 standard; DNA; 9905 BP.
 XX
 AC AAK98324;
 XX
 DT 30-APR-2002 (first entry)
 XX
 DE Human purinergic-related G-protein coupled receptor (GPCR) genomic DNA.
 XX
 KW Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
 KW signal transduction; human protease; GPCR disorder; gene therapy;
 KW transgenic animal; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT replace (6613, T)
 FT /*tag- a
 FT replace (7738, G)
 FT /*tag- b
 FT replace (7732, C)
 FT /*tag- c
 FT 8309..9322
 FT /*tag- d
 FT /number= 1
 FT 8309..9322
 FT CDS
 FT /*tag- e
 FT /product= "G-protein coupled receptor"
 PD W0200187980-A2.
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US15957.
 XX
 PR 18-MAY-2000; 2000US-205196P.

PR 08-AUG-2000; 200005-0634656.
 XX (APPL-) APPLERA CORP.
 PI Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
 XX WPI; 2002-075312/10.
 DR P-PSDB; AAO14027.
 XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterised by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies
 XX
 PS
 XX Claim 23; Fig 3; 64p; English.

XX The present specifically claimed human genomic DNA sequence (located on
 CC chromosome 13) encodes a putative G-protein coupled receptor
 CC (GPCR) of the invention. GPCRs constitute a major class of proteins
 CC responsible for signal transduction within a cell. Upon binding of a
 CC ligand to the extracellular portion of a GPCR, a signal is transduced,
 CC resulting in a biological or physiological change within the cell. The
 CC GPCR proteins can be divided into five families, family I contains the
 CC putative GPCRs (e.g. the P2Y receptors). P2Y receptors are
 CC characterised by their selective responsiveness towards ATP and its
 CC analogues, some also respond to UTP. The invention comprises a human
 CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR
 CC protein and nucleic acids of the invention are useful in the treatment of
 CC a disease or condition mediated by a human protein. The GPCR protein of
 CC the invention is useful for the development/identification of
 CC therapeutic proteins; assays designed to quantitatively determine levels
 CC of the protein in biological fluids; identifying compounds which modulate
 CC the activity of the GPCR, or the interaction of the GPCR and a molecule
 CC with which it normally interacts; and treating a disorder characterised
 CC by an absence of, or inappropriate expression of the GPCR protein. The
 CC GPCR nucleic acids of the invention are useful in: diagnostic assays to
 CC identify changes in the GPCR nucleic acid that lead to pathology;
 CC controlling GPCR expression; and in gene therapy to treat patients with
 CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
 CC the production of transgenic animals.
 XX

SO Sequence 9905 BP; 2656 A; 2218 C; 2061 G; 2970 T; 0 other;

Alignment Scores:

Pred. No.: 8.37e-144 Length: 9905
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775b-2 (1-337) x AAK98324 (1-9905)

QY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerSphProAspTyrAlaAla 20
 DB 8309 ATGAAATGAGCAGCTAGCTATTTAGCAAAAGCTTCTGATTTCCCGATTTAGCGCTGCT 8368
 QY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuIleuMetHisTyrLeuProValIleTyr 40
 DB 8369 TTGGAAATGAGCAGCTAGCTATTTAGCAAAAGCTTCTGATTTCCCGATTTAGCGCTGCT 8428
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 8429 GGCATTAATCTCTCCGCGGATTTCCAGCAATGCACTAGTATGATACACTTACATTTTC 8488
 QY 61 LysMetArgProIlePheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 8489 AAATATGAGCAGCTTGGAGAGCAGCAGCATCATTAATGCTGAACCTGGCTCAGCAGATCTG 8548
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
 DB 8549 CTGTATCTGACGACGCTCCCTTCCTGATTTCACTACTATGCGCAGTGGCAAAACTGATC 8608

QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 8609 TTGGAGATTTTCATGTAAGTATATCCGGCTTCAGCTTCCATTTCAACAGCTGATACAGC 8668
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
 DB 8669 ATCTCTTCCTCCACCTGCTTTCAGCATCTTCGCTACCTGCTGATGATCAATTCACCAATGAGC 8728
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaValIleValIleTyrIleIle 160
 DB 8729 TGCCTTTCCATTCACAAACTCCATGTCAGCTTGTACCTGCTGCTGCTGCTGATAT 8788
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 8789 TCACGTGATGTCATCCGATGACGATGACCTCTTGATCATCAACCAACAGACAGACAGA 8848
 QY 181 SerIleAsnLeuAspLeuThrSerSerAspGluLeuAsnThrIleTyrIleTyrAsnLeu 200
 DB 8849 TCACCTGCTGCTCCGACCTCAGCAGATTCGATGAACTCAATCTTAAGTGTACCAACCTG 8908
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValIleThrLeuCysTyrThrThr 220
 DB 8909 ATTTGACTGCACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8968
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlyGlnAlaArg 240
 DB 8969 ATATTCACACCTGACCCATGACCTGACCTCAACCTGACCTGACCTGACCTGACCTGACCTGAC 9028
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 9029 AGGTAAACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9088
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 9089 AGGTATCTGAGATCGAATCTCCGCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 9148
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 9149 CATGAACCTTACATCATCTTCTGACCATTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9208
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValIleCysSerThrValArgCysLys 320
 DB 9209 CTATATGTGTGGTGCAGCAGCAACTTTCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9268
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 9269 GTAAGCGGGAACCTTGAGCAAGCAAAATAATTAGTTACTCAAAACACCT 9319

RESULT 12
 ID AAS08362 standard; cDNA; 1729 BP.
 XX AAS08362;
 AC AAS08362;
 XX 26-SEP-2001 (first entry)
 DE Human cDNA encoding G-protein coupled receptor, GPCR 39404.
 KW Human; G-protein coupled receptor; GPCR; 39404; immunogen; antibody;
 KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;
 KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
 KW systemic lupus erythematosus; actinic keratosis; myocardiitis;
 KW Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasm;
 KW inflammations; teratoma; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 294..1307
 FT CDS
 FT /product= "protein 39404"
 XX PN W0200149847-A2.

XX 12-JUL-2001.
 PD 22-DEC-2000; 2000MO-US35309.
 XX 30-DEC-1999; 9905-0475790.
 PR (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA, white D;
 XX WPI: 2001-432880/46.
 DR P-PSDB: AA004584.
 XX
 PT Novel isolated 26904, 38911 and 39404 polypeptides which are seven
 PT transmembrane proteins belonging to superfamily of G-protein-coupled
 PT receptors, useful for treating disorders of spleen, lung, liver, brain
 PT and kidney -
 XX
 PS Claim 2: Fig 1; 164pp; English.

XX The sequence encodes a novel human seven transmembrane domain
 CC protein belonging to the G-protein coupled receptor (GPCR) superfamily,
 CC protein 39404. The receptor is useful in drug screening assays, to
 CC identify compounds that modulate receptor activity and/or interact with
 CC the receptor, and for producing antibodies specific for the receptor, its
 CC regions or fragments. The receptor is useful for treating/diagnosing a
 CC 26904, 38911 and 39404 protein-associated disorder characterized by
 CC aberrant expression or activity of the protein, for monitoring
 CC therapeutic effect during clinical trials and other treatment, as bait
 CC analysis in a two-hybrid or three-hybrid assay, and in pharmacogenomic
 CC analysis. The proteins and nucleic acids encoding them are useful for
 CC diagnosis and treatment of disorders selected from disorders of the
 CC spleen, lung such as Good pasture's syndrome, liver such as viral
 CC hepatitis, brain such as Alzheimer's disease, hematopoietic stem cells
 CC such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
 CC disease, colon such as Crohn's disease, uterus and endometrium such as
 CC endometriosis, T-cell disorders such as systemic lupus erythematosus,
 CC diseases of the skin such as actinic keratosis, disorders of the heart
 CC such as myocarditis, disorders involving blood vessels such as Kawasaki
 CC syndrome, disorders involving the thymus such as DiGeorge syndrome,
 CC disorders involving B-cells such as peripheral B-cell neoplasms,
 CC disorders of the breast such as inflammations, and disorders involving
 CC the testis and epididymis such as teratoma. Numerous examples of
 CC each type of disorder are given in the specification.

XX Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;

Alignment Scores:

Pred. No.: 3,91e-144 Length: 1729
 Score: 1764.00 Matches: 336
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 22 Gaps: 0

US-10-023-775b-2 (1-337) x AAS08362 (1-1729)

QY 1 MetaangluProleuaspTyrleuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 294 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGATTCGCCGATTATGAGCTGT 353
 QY 21 PheglyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 354 TTGGAAATTCACGATGCAAAACATCCACACACATGATCCTCCCTGTTATTATAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 414 GGCATTATCTCTCTGCTGGGATTTCCAGCAATGCGATGATATCCACTTACATTTC 473
 QY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 474 AAAATGAGACCTTGGAGAGAGACACATCATTTATGCTGACCTGCGCAGACATCTG 533

QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
 DB 534 CTGTATCTACACAGCCTCCCTTCCTGATTCACCTACTATAGCCAGTGGCAAACTGATC 593
 QY 101 PheglyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 594 TTGGAGATTTATGATGTAAGTTATCCGCTCAGCTTCATTCATTCACCTGATACGAC 653
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 654 ATCCCTTCCTCACCCTGTTTCAGCATCTCCGCTACTGCTGATTCATTCACCAAGGAC 713
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaIleCysAlaValAlaTyrIleIle 160
 DB 714 TCGTTTTCATTCACAAACCTGATGTGAGTTGACCTGCTGCTGCTGATTCATTC 773
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgTyrAsnArg 180
 DB 774 TCACCTGTAGCTGTATTCATTCGATGACCTTCCTTCATCATCAACCAAGGACACAG 833
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
 DB 834 TCAGCCTGTCTGACCTCACCAGTTCGATGAACTCAATATTAATGATGACCAACTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 894 ATTTTACGCAACTCTTCTGCTCCCTTGCTGATATGACACTTGTCTATACACG 953
 QY 221 IleIleHisThrLeuThrThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 954 ATTATCCACACCTGTGACCATGAGTGCAGAACTGACAGAGCTTATGAGCAAGACAG 1013
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTTACCATCTCTGCTACTCTTCATTTAGTATGTTTATACCTTCATATCTTG 1073
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGCTATTCGATGCAATCTGCTGCTTTCATATGATGTTGATGCAATTCAGATC 1133
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 1134 CATGAAGCTTACATGCTTCTTGAGCATTAGCTGCTGAGAACCTTGTGATACCTGTTA 1193
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 1194 CTATATGTGTGTGTCAGCACAACCTTTCAGCAGGCTGTCTGCTCAACAGTGAATCMAA 1253
 QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 1254 GTAAAGGGAGAACCTTGAGCAAGCAAAAGAAATTAATTACTCAAAACACCT 1304

RESULT 13
 ABV24026
 ID ABV24026 standard; cDNA; 1729 BP.
 XX
 AC ABV24026;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 24017.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US05171.

XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PS Claim 1; Page 4453-4454; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Alignment Scores:
 Pred. No.: 3,91e-144 Length: 1729
 Score: 1764.00 Matches: 336
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 23 Gaps: 0
 US-10-023-775b-2 (1-337) x ABV24026 (1-1729)
 QY 1 MetasngluProleuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 294 ATGAATGAGCCACTAGACTATTTAGCAAAATGCTTGTATTTCCCGATTAAGACGCTGCT 353
 QY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuIleuMetHisTyrLeuProValIleTyr 40
 DB 354 TTGGAAATTCGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 414 GGCATATTCCTCCGCGGATTTCCAGCAATGCACTAGATGATCCACTTACATTTTC 473
 QY 61 LysMetArgProTrpPheLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 474 AAAATGAGACCTTGGAAGACACACCATCATTAATGTGAACCTGGCCTGCACAGATCTG 533
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
 DB 534 CTGTATTCGACGACCTCCCTTCCTGATTCACACTACATGACGACGCGAAGAACTGATC 593
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 594 TTGGAGATTTCAATGTTAGTTATCCGCTTCAGCTTCATTTCAACCTGTAATAGACG 653
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140

DB 654 ATCCTCTCCCTACCTGTTTCAGACATCTCCGCTACCTGTGATCATCCCAATGAGC 713
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaIleCysAlaValAlaTyrPheIle 160
 DB 714 TGCCTTTCCATTCCAAAACCTCGATGCTGCACTGTGTACCTGTGTGTGTGATCATTT 773
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 774 TCACGTGTACCTGTGATCCGATGACCTTCTTGTATCATCAACCAACGACGACGACG 833
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPheAsnLeu 200
 DB 834 TCAGCCCTGCTCGACCTCCACAGCTCGAGTGCAGTCAATCACTAATTAAGTGTACAACTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValPheLeuCysTyrThrThr 220
 DB 894 ATTTTGACCTGCAACTCTTCTGCTCCCTTGATGATGACACTTGTCTATACGACG 953
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlyAlaArg 240
 DB 954 ATATCCACACTGTGACCCCATGAGCTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGCA 1013
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTAACCATTTGCTACTCTCTGCACTTTAGCTATGTTTATACCTTCATATCTTG 1073
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGCTCTTGTGATCGAATCTCCGCTCTTCAATCACTGATGATGATGATGATGATG 1133
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 1134 CATGAAGCTTACATCGTTCTGTGACCATTAAGCTGCTGAAACACTTGGTAACTGCTTA 1193
 QY 301 LeuTyrValValValSerAspAsnPheGlnAlaValAlaLysSerThrValArgCysLys 320
 DB 1194 CTATATGTGTGTGTCACGACGACACTTTCACAGGCTGTCTGCTCAACAGTGAAGTGA 1253
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysIleSerTyrSerAsnAsnPro 337
 DB 1254 GTAAAGCGGAACCTTGAGCAAGCAAAATAATTAGTACCAAAACACCT 1304
 RESULT 14
 ID ABV25767 standard; cDNA; 1729 BP.
 XX
 AC ABV25767;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25758.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR MPI: 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX

PS Claim 1: Page 5175-5176; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other:

Alignment Scores:

Score:	3.91e-144	Length:	1729
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Query Match:	99.70%	Mismatches:	1
DB:	23	Indels:	0
		Gaps:	0

US-10-023-775B-2 (1-337) x ABV25767 (1-1729)

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 DB 294 ATGAATGAGCCACTGACATTTTACCAATGCTTGATTCGCCGATATACAGCTGCT 353
 QY 21 PheGlyAsnCySerAspGluAsnLeuProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 354 TTGGAAATGTCACATGATGAAGAAACATCCACATCAAGATGACCTACCTCTGTATTAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 414 GGCATTATCTCTCGTGGGATTCAGCAGATGAGATGATATCCACTTACATTTTC 473
 QY 61 LysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
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 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile 100
 DB 534 CGTGATCTGACAGCCTCCCTCTCTGATTCACCTATGATCCAGAGTGGCAAAACGTGATC 593
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 594 TTTGGAGATTTCATGTAAGTTTATCCGCTTACCTTCCACTTCAACCTGTATAGCAC 653
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 DB 654 ATCCCTTCCTCACCCTGTTTCAGCATCTTCCGCTACTGTGATCATCAACCAACGAGAC 713
 QY 141 CysPheSerIleHisTyrArgCysAlaValAlaCysAlaValAlaTyrPileIle 160
 DB 714 TGCCTTTCCATTCACAAAACCTGATGTCAGTTGAGCTGTGCTGTGGATCATT 773
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 774 TCACGTGATGCTGATTCGATGACCTTCTTGATCACAATCAACCAAGAGCAACAGA 833

QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
 DB 834 TCAGCTGTCTGACCTCACCACACTGGAGAACTCAATATTAAGTGTACCACTG 893
 QY 201 IleLeuThrAlaThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 894 ATTTGACGCAACATCTTCTGCGCCCTGCTGATAGTACACTTGTATACACAG 953
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 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
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 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
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 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 1194 CTATATGTGTGTGTGACGACCAACTTTCAGACAGCTGTCTGCAACAGTGAATGCMAA 1253
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 DT 16-SEP-2002 (first entry)
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 DE Human prostate expression marker cDNA 29900.
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 KW pharmacogenomic marker; gene; ss.
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 OS Homo sapiens.
 XX
 PD 23-AUG-2001.
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 PD 20-FEB-2001; 2001WO-US05171.
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 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 PR
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR MPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 6451; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1729 BP: 461 A; 401 C; 302 G; 548 T; 17 other;

Alignment Scores:

Pred. No.:	3,91e-144	Length:	1729
Score:	1764.00	Matches:	336
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.60%	Indels:	0
B:	23	Gaps:	0

US-10-023-775b-2 (1-337) x ABV29909 (1-1729)

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 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 354 TTGGAATATGACATGATGAAGAACATCCACTCAAGATGACACTGCTCCGTTATTAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 414 GGCATTATTCCTCTGCTGGGATTTCCAGGCAATGCAATGATATCCACTTACATTTTC 473
 QY 61 LysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 474 AAAATGAGACCTTGGAGAGAGCAGCAGCATTTATGCTGAACCTGGCCCTGCAGATCTG 533
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTyrPle 100
 DB 534 CTGATCTGACACACCTCCCTTCCTGATTCACTATGACAGTGGGAAACTGATC 593
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 120
 DB 594 TTGGAAGATTTCATGTAGTTATCCGCTTCAGCTTCCATTCCAACTGTATAGCAGC 653
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
 DB 654 ATCCTCTTCTCCTACCTGTTTCAGCATCTTCGGTACTGTGATGATTCACCCATAGAGC 713
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrPleIle 160
 DB 714 TGCCTTTCATTCACAAACTCGATGATGAGAGTTTACCTGCTGTGGTGTGATCAT 773
 QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgTyrAsnArg 180
 DB 774 TCACCTGTACTGATTCGATGATGACCTTCTTGATTCATCAACCAAGAGCAACAGA 833
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrAsnLeu 200
 DB 834 TCAGCCGTCTGACCTCAGCAGCAGTTCGATGAGAACTCAATATTAAGTGTACAACTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 894 ATTTGACTGCACTACTTCTGCTCCCTGTGTGATAGTACACTTTGCTATACACAG 953
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240

DB 954 ATATTCACACTCTGACCCATGACATGCAAACTGACAGCTGCCTTAAGCAGAAAGCAGCA 1013
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTAACATTCGCTACTCTTGCATTTAGCTATGTTTATACCTTCCATATCTTG 1073
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGTCATTCGATGATGCAATCTCGCTGTTCAATCAGTTGTCCATTTGAGAAATCAGATC 1133
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleLeuAsnThrPheGlyAsnLeu 300
 DB 1134 CATGAGCTTACATCGTTTCTGAGCAATTAAGTCTGCTGAAACCTTTGGTAACTCTGTA 1193
 QY 301 LeuTyrValValIleSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 1194 CTATATGTGTGTGTCAGCAGCAACTTTCAGAGGCTGTCTGCTCAACAGTATGACAAA 1253
 QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 1254 GTAAGCGGGAACCTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTT 1304

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 23:11:00 ; Search time 3126 Seconds

(without alignments)
3137.443 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1771	100.0	1014	6 AX384211	AX384211 Sequence
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18	597	33.7	2245	6 AX384210	AX384210 Sequence
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RESULT 1

ALIGNMENTS

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LOCUS AX148186 1014 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 27 from Patent WO0136471.
ACCESSION AX148186
VERSION AX148186.1 GI:14347086
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1014)
Chen, R., Dang, H.T. and Lowitz, K.P.
Endogenous and non-endogenous versions of human g protein-coupled
receptors
Patent: WO 0136471-A 27 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
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DEFINITION Sequence 10 from Patent WO0187937.
ACCESSION AX305130
VERSION AX305130.1 GI:17644765
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Batterson, C., Lu, D.A., Thornton, M., Lu, Y., Tribouley, C.M.,
Graul, R., Khan, F.A., Ganahl, A.R., Walla, N.K., Nguyen, D.B., Yue, H.,
Hafalla, A., Elliott, V.S., Lal, P., Reddy, R., Kallick, D.A., Tang, T.Y.
and Au-Young, J.
G-protein coupled receptors
Patent: WO 0187937-A 10 22-NOV-2001;
Incyte Genomics, Inc. (US)
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/db_xref="taxon:9606"
/note="Incyte ID No: 6575963CB1"
BASE COUNT 259 a 263 c 188 g 304 t
ORIGIN
Alignment Scores:
Pred. No.: 1.32e-126 Length: 1014
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrlleuProValIleTyr 40
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 DEFINITION Sequence 1 from Patent WO0187980.
 ACCESSION AX379468
 VERSION AX379468.1 GI:19575226
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Wei, H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and

TITLE Beasley, E.M.
 JOURNAL Isolated human g-protein coupled receptors, nucleic acid molecules
 Patent: WO 0187980-A 1 22-NOV-2001;
 Applera Corporation Robert A. Millman Assistant Secretary (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Ramakrishnan S.
AUTHORS Regulation of human p2y1-like g protein-coupled receptor
TITLE Patent: WO 0214511-A 5 21-FEB-2002;
JOURNAL Bayer Aktiengesellschaft (DE)
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Alignment Scores:
Pred. No.: 1,32e-126 Length: 1014
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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DB 241 CTGTATCTGACACGCTCCCTCCCTGATTCATCTACTATGCGCGAGTGGCAAAACTGATC 300
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OY 301 LeuTyrValIValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
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VERSION AX464561.1 GI:21899357
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Fiddock M.D.
AUTHORS G-protein coupled receptors having homology to the p2y
TITLE purinoreceptor 1 (p2y1)
JOURNAL Patent: EP 1219638-A 1 03-JUL-2002;
Pflizer Limited (GB) ; Pflizer Inc. (US)
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Pred. No.: 1,32e-126 Length: 1014
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 REFERENCE
 1
 Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.
 Identification of G protein-coupled receptor genes from the human
 genome sequence
 Unpublished
 2 (bases 1 to 1014)
 Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.
 Direct Submission
 Submitted (10-APR-2002) Shigeaki Takeda, Gunma University,
 Department of Biological and Chemical, Engineering, Faculty of
 Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan
 (E-mail:stakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434,
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REFERENCE 2 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantli,W.B., Arkhitko,O.,
TITLE Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
JOURNAL Direct Submission
Submitted (17-AUG-2001) Department of Pharmacology, University of
Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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Pred. No.: 1,32e-126 length: 1014
Score: 1771.00 Matches: 337
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
Gaps: 0
US-10-023-775b-2 (1-337) x AF411109 (1-1014)
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Qy 61 LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
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Db 361 ATCTCTTCCTCCACCGCTTTCACACATCTCCGCTACGTGTGATCATTCACCAATAGC 420
Qy 141 CysPheSerIleHisTyrThrArgCysAlaValAlaIaCysAlaValAlaTrpIleIle 160
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 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
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 Db 961 GTAGCGGGAACCTTGAGCAAGCAAGAAATTTAGTACTCAACCAACCCCT 1011
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 AX458238
 LOCUS AX458238 1081 bp DNA linear PAT 08-JUL-2002
 DEFINITION Sequence 1 from Patent WO0246414.
 ACCESSION AX458238
 VERSION AX458238.1 GI:21724972
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and
 Rysek, R. P.
 TITLE A novel human g-protein coupled receptor, hgrbmy23, expressed
 highly in kidney
 Patent: WO 0246414-A 1 13-JUN-2002;
 Bristol-Myers Squibb Company (US)
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 BASE COUNT 280 a 277 c 198 g 326 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1,41e-126 Length: 1081
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
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 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTrpIle 100
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 Db 294 CTGATATGACACACCTCCCTCTCTGATTTACTACTATGACATGCGAGTGGGAATCGATC 353
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
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 Db 354 TTTGAGATTTTCAATGTGTAACTTTATACCGCTTCAAGCTTTCATTTCAACCTTATAGCAGC 413
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
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 QY 181 SerAlaCysLeuAspLeuThrSerSerAspIleuAsnThrIleLeuSTrPtyrAsnLeu 200
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 Db 594 TCAGCTGTCTCGACCTGACAGTGGATGAACTCAATATATTAAGTGTACACCTG 653
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Db 954 CTATATGTGTGGTCAGCGACACTTTCAGCAGCGCTGTCTGCTCAACAGTGAATGCAAA 1013

QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
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Db 1014 GTAGCGGGAACCTTGAGCAAGCAAGAAATAGTACTCAACAAACCT 1064

RESULT 9
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LOCUS Homo sapiens G protein-coupled receptor GPR99 (GPR99) mRNA,
DEFINITION complete cds.
ACCESSION AF370886
VERSION AF370886.1 GI:21728283
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1092)
AUTHORS Wittenberger,T., Hellebrand,S., Munck,A., Krelenkamp,H.J.,
Schaller,H.C. and Hampe,W.
GPR99, a new G protein-coupled receptor belonging to a new subgroup
of nucleotide receptors
BMC Genomics 3 (1), 17 (2002)
JOURNAL 12098360
PUBMED 2 (bases 1 to 1092)
REFERENCE Hampe,W.
AUTHORS Direct Submission
TITLE Submitted (17-APR-2001) Developmental Neurobiology, Zentrum fuer
JOURNAL Molekulare Neurobiologie, Martinistr, Hamburg 20246, Germany
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19. 1032
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BASE COUNT 290 a 279 c 198 g 325 t

ORIGIN

Alignment Scores:
Pred. No.: 1.43e-126 Length: 1092
Score: 1771.00 Matches: 337
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
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RESULT 10
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LOCUS Homo sapiens gene for seven transmembrane helix receptor, complete
DEFINITION cds, isolate:CBRC7M_440.
ACCESSION AB065877
VERSION AB065877.1 GI:21929018
KEYWORDS
SOURCE Homo sapiens (isolate:CBRC7M_440) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
Teutsuhl,S., Aburatani,H., Asai,K. and Akiyama,Y.

TITLE Genome-wide discovery and analysis of human seven transmembrane helix receptor genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1414)
AUTHORS Suwa,M.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST): 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/, Tel:81-3-3599-8080, Fax:81-3-3599-8081)

COMMENT This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated finding(GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.
And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo].

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CDS
BASE COUNT 376 a 337 c 260 g 441 t
ORIGIN

Alignment Scores:
Pred. No.: 1.87e-126 Length: 1414
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-023-775B-2 (1-337) x AB065877 (1-1414)

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QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
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QY 261 ArgValIleArgIleLeuSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
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QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
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DB 1101 CTATATGCTGTGCTGACGACCAACTTTCAGCAGGCTGCTGCTCAACAGTATGATCA 1160
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RESULT 11
AX379470
LOCUS AX379470 9905 bp DNA linear PART 18-MAR-2002
DEFINITION Sequence 3 from Patent WO0187980.
ACCESSION AX379470
VERSION AX379470.1 GI:19575227
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wei,M.H., Zhao,Q.C., Cravchik,A.C., di Francesco,V.C. and Beasley,E.M.
TITLE Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof
JOURNAL Patent: WO 0187980-A 3 22-NOV-2001;
Applera Corporation Robert A. Millman Assistant Secretary (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 2656 a 2218 c 2061 g 2970 t
ORIGIN

Alignment Scores:

Pred. No.: 1.41e-125 Length: 9905
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 100.008 Indels: 0
 DB: 6 Gaps: 0

US-10-023-775b-2 (1-337) x AX379470 (1-9905)

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Db      8549 CTGATATCGACACGCTCCCTTCCTGATTCACACTACTACTGCGACGAAACTGATC
QY      101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
Db      8609 TTGGGAGATTTCAGTGTAGTTATCCGCTTCACTGCTTCAACCTGATATGACG
QY      121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
Db      8669 ATCTCTCTCTCCACCTGTTTACACATCTCCGCTACGTGTGATCATTCACCCAAATGAGC
QY      141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrIleIle 160
Db      8729 TCGTTTTCATTCACAAACTCATGATGCGATGTCGCTGCTGCTGCTGCTGATCAT
QY      161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db      8789 TCACCTGATGCTCTCATTCGAGACCTCTTATCATCAACCAACAGACCAACAGACA
QY      181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
Db      8849 TCAGCTGTCTGCACCTCCACACCTCGGATGAACTCAATACTAATTAAGTGTACAACTG
QY      201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db      8909 ATTTGACGTCACACTACTTCTGCTCCCTGCTGTGTATGACACTTCTCTATACACG
QY      221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
Db      8969 ATTATTCACACTCTGACCCATGAGACGCAACTGACGCTGCTTAAAGCAAGACGACA
QY      241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
Db      9029 AGGCTTAACCACTTGTCTGCTACTCTTGCATTTTACGATGTTTACCTTCCATATCTTG
QY      261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db      9089 AGGGTCAATTCGATCGAATCTGCGCTTCAATCACTGTTCCATTCATGGAATCAGATC
QY      281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
Db      9149 CAGGAGCTTACATCTTCTTACACATTAAGTGTCTGAAACACTTGTGTAACCTGTA
QY      301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
Db      9209 CTATATGTGTGTGTGAGCGACCAACTTTCACAGAGCTGTCTGCTCAACAGTGAATGCAAA
  
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QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAspPro 337
 Db 9269 GTAAAGCGGAACTTGAGCAAGCAAAATAATTGTTACTCAACCAACCT 9319

RESULT 12
 AL356486/C
 LOCUS
 DEFINITION Human DNA sequence from clone RP11-721F14 on chromosome 13, complete sequence.

ACCESSION AL356486 67645 bp DNA linear PRI 28-SEP-2001
 VERSION AL356486
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 67645)

COMMENT Direct Submission
 Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Sep 28, 2001 this sequence version replaced gi:15787734.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 13, constructed by the Sanger Centre Chromosome 13
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/RGP/Chr13>

RP11-721F14 is from the library RPCI-11.3 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/dacpac/home.htm>
 VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone
 RP11-721F14. It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.
 The true left end of clone RP11-199B17 is at 65646 in this
 sequence. The true right end of clone RP11-651J9 is at 2000 in this
 sequence.

FEATURES
 source location/Qualifiers

1..67645
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="13"
 /clone="RP11-721F14"
 /clone_1b="RPCI-11.3"
 53919
 misc_feature
 /note="Random repeat. Forced join. Gap size estimated to
 be approximately 110bp by restriction digest data."

BASE COUNT 20542 a 13252 c 13216 g 20635 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.04e-124 Length: 67645
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.008 Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-023-775b-2 (1-337) x AL356486 (1-67645)

OY 1 MetanigluProleuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
DB 5091 ATGAAATGAGCCATGACTATTAGCAAAATGCTTGTATCCCGATTATGACCTGCT 5032
OY 21 PheGlyAsnGlySerAspGluAsnLeuProleuGlyMetHisTyrLeuProValIleTyr 40
DB 5031 TTGGAAATGTCACATGATGAAACATCCACTCAAGATGACACTACCTCCCTGTTAT 4972
OY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
DB 4971 GGCATATCTCTCTGCTGGATTTCCAGCAATGAGATGATATCCACTTACATTTTC 4912
OY 61 LysMetArgProTyrPheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
DB 4911 AAAATGAGACCTTGGAAAGAGACGACCATCATTTAGTGAACCTGCGTGCACATCTG 4852
OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
DB 4851 CTGATCTGACACGCTCCCTCTGCTGATCTACTATGCGACAGTGGCAAAACTGATC 4792
OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 120
DB 4791 TTGGAGATTTTCATGTGATGATTTATCCGCTTACCTTCACCTTCACCTGATAGCAGC 4732
OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
DB 4731 ATCCCTCTCCACCTGCTTACAGCATCTCCGCTACTCTGATCATCTCACCACATGAGC 4672
OY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrIleIle 160
DB 4671 TGCCTTTCATTCACAAACTGAGATGTCAGTGTGAGCTGCTGCTGCTGATCAT 4612
OY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
DB 4611 TCACGTGATGCTGATTCATTCAGATGACCTTGTGATCATCATCAACACAGGACCAACGA 4552
OY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrTyrAsnLeu 200
DB 4551 TCACGCTCTCTGACACTGACACGATGCGATGATCACTCATTAATGATGACACCTG 4492
OY 201 IleLeuThrAlaThrThrPheCysLeuProleuValIleValThrLeuCysTyrThrThr 220
DB 4491 ATTTTGACTGCAACTACTTCTGCTCCCTGCTGGATGATGACACTTGTGATACACAG 4432
OY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
DB 4431 ATTATTCACACTGTCACCATGACACTGCAAACTGACACTGCTTACACAGAACACAGA 4372
OY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
DB 4371 AGGCTAACCATCTGCTACTCTGCTGATTTACGATGATTTTATTCCTTCATATCTTG 4312
OY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
DB 4311 AGGGTCATTCGAGATGATTCGCGCTGCTTCAATCACTTGTTCATTTGAGATACAGATC 4252
OY 281 HisGluAlaTyrIleValSerArgProleuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
DB 4251 CATGAAAGCTTACATCGTTTTCAGACATGATGCTGCTGCAACACCTTGTGTAACCTGTTA 4192
OY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
DB 4191 CTATATGTGTGTGTCAGCAGCAACTTTCAGCAGGCTGTCTGTCAACAGTGTGATGCANA 4132
OY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
DB 4131 GTAAGCGGACCTTGACCAAGCAAAAGAAATTTGTTACTCAAAACACCT 4081

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RESULT 13
AC026756
LOCUS
AC026756
DEFINITION
AC026756
VERSION
AC026756.15
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 156555)
REFERENCE
AUTHORS
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedeerspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
Direct Submission
Submitted (23-MAR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
2 (bases 1 to 156555)
REFERENCE
AUTHORS
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedeerspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
Direct Submission
Submitted (23-FEB-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
3 (bases 1 to 156555)
REFERENCE
AUTHORS
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedeerspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
Direct Submission
Submitted (23-FEB-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
On Feb 23, 2001 this sequence version replaced gi:12745089.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDBTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum.info@sequence.stanford.edu
----- Project Information
Center project name: 870
Center clone name: RP11-286P8
----- Summary
This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
FEATURES
source
Location/Qualifiers
1..156555
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-286P8"
/clone_11b="RP11 human BAC library 11"
BASE COUNT
48748 a 30845 c 30755 g 46207 t
ORIGIN
Alignment Scores:
Pred. No.: 2,49e-124 Length: 156555
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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DB: 9 Caps: 0

US-10-023-775b-2 (1-337) x AC026756 (1-156555)

OY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20

DB 140188 ATGAATGAGCCTAGACTATTATTAAGCAAAATGCTTCGATTTCCCGGATTAATGAGCTGCT 140247

OY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40

DB 140248 TTGGAAATTCAGCTGATGAAACATCCCAAGTGCACATACCTCCCTGTTATTTAT 140307

OY 41 GlyTllePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrTllePhe 60

DB 140308 GGGATTATCTTCCTCGGGGATTTCCAGGCAATGCAAGTATGATTCACATTCATTTTC 140367

OY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnIleuAlaCysThrAspLeu 80

DB 140368 AAAATGAGACCTTGGAAAGACACACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 140427

OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile 100

DB 140428 CTGTACTGACAGCCTCCCTCCCTGATTCACATACATCCAGTGGCGAAACTGATC 140487

OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120

DB 140488 TTGGAGATTTCATGTTAGTTATCCGCTCAGCTTCATTCACCTGTTATAGCAGC 140547

OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140

DB 140548 ATCCCTTCTCCTCAGCTGTTTCACACATCTTCGCTACGTCGTGATTCACCAAGAGC 140607

OY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrPileIle 160

DB 140608 TGCTTTTCATTCACAAACTCATGATGAGCTGTGAGCTGCTGCTGGTGGATCAT 140667

OY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180

DB 140668 TCACCTGTCAGCTGTCATTCGGAAGACCTTCCTATCACAACCAACAGACAGCAGCA 140727

OY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200

DB 140728 TCAGCTGCTCAGCTCAGCAGCACTGAGTGAATCATATCTTTAAGTGTGACAACTG 140787

OY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220

DB 140788 ATTTGACTGCACTACTTCTGCTCCCTGCTGATGATGACACTTTCCTATACACAG 140847

OY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240

DB 140848 ATTATCCACACTGTCAGCCATGAGCAAACTGACAGCTGCCCTTAAGCGAAAGCGCA 140907

OY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260

DB 140908 AGGCTACCATTTGCTACTCCTTGCATTTTACGTATGTTTTTACCTTCCATATCTTG 140967

OY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280

DB 140968 AGGCTATTCGATGCAATCTCCCTGCTTCAATCAGTTGTTCCATGGAATGATGATC 141027

OY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300

DB 141028 CATGAAGCTTACATCTTCTTACACCATTAAGCTGCTGCAACACTTGGTAACTGTGA 141087

OY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320

DB 141088 CATATGTCGTGCTGACCAACACTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA 141147

OY 321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTyrSerAsnAsnPro 337

DB 141148 GTAAAGGGAGACCTTGAGCAGCAAGAAATTAAGTTACTCAAAACACCT 141198

RESULT 14

AX191332
LOCUS AX191332 1729 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 2 from Patent WO0149847.
ACCESSION AX191332
VERSION AX191332.1 GI:15209582
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Glucksmann, M.A. and White, D.
TITLE 26904, 38911, and 39404, seven-transmembrane proteins / g-protein coupled receptors
JOURNAL Patent: WO 0149847-A 2 12-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1..1729
/organism="Homo sapiens"
/db_xref="taxon:9606"
294..1307
/note="unnamed protein product"
/codon_start=1
/protein_id="CA51133.1"
/db_xref="GI:15209583"
/translation="MNEPLDYLANSDPDDYAAFGNCNDENIPLMKHYLPVYGIIF
LVFPGNAVIVSYIFKMPKWSSTIMLACTDLVLSPLFHHYVAGSNWJG
DFMCRIRSEFHNLSILFLCFSEFRVCYIIHMSGSIKTKCAVACAVMI
LSAVIIPMFELISTNTNRSACLDLSSDELMITKYNLILATFPCLPVITVY
TTIIRHILHQLQDSCLKOKARLLTILLIATFVCLPPIIILVIRIESLSSSI
ENQIHRAVIVSGPLALNFTGNLLTVVSDNFOAVSTVCKVSGNLEQAKKIST
NRP"
BASE COUNT 461 a 403 c 302 g 563 t
ORIGIN
Alignment Scores:
Pred. No.: 7.88e-126 Length: 1729
Score: 1764.00 Matches: 336
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 6 Gaps: 0

US-10-023-775b-2 (1-337) x AX191332 (1-1729)

OY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20

DB 294 ATGAATGAGCCTAGACTATTATTAAGCAAAATGCTTCGATTTCCCGCATTATGAGCTGCT 353

OY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40

DB 354 TTGGAAATTCAGCTGATGAAACATCCCAAGTGCACATACCTCCCTGTTATTTAT 413

OY 41 GlyTllePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrTllePhe 60

DB 414 GGGATTATCTTCCTCGGGGATTTCCAGGCAATGCAAGTATGATTCACATTCATTTTC 473

OY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnIleuAlaCysThrAspLeu 80

DB 474 AAAATGAGACCTTGGAAAGACACACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 533

OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile 100

DB 534 CTGTACTGACAGCCTCCCTCCCTGATTCACATACATCCAGTGGCGAAACTGATC 593

OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120

DB 594 TTGGAGATTTCATGTTAGTTATCCGCTCAGCTTCATTCACCTGTTATAGCAGC 653

OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140

DB 654 ATCCCTTCTCCTCAGCTGTTTCACACATCTTCGCTACGTCGTGATTCATTCACCAATGAGC 713

QY 141 CyspserIleHisIysThrArgCysAlaValAlaCysAlaValAlaIleIle 160
 DB 714 TCCCTTTCATTCACAAAACGCGATGTCAGTTGAGCCCTGCTGTGGTGGATCAT 773
 QY 161 SerLeuValAlaValIlePromethrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 774 TCACGGTGAAGCTGATTCGATCCGATGACCTTGTGATCAATCAACACGAGGACCAACGA 833
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleIleStryPyrAsnLeu 200
 DB 834 TCAGCTGTCTGCGACCTACACGATGCGATGACATCAATTAATGATGATCAACCTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysThrThrThr 220
 DB 894 ATTTGAGCTGCAACTTCTTCCCTCCCTGGATGATGATGATGATGATGATGATGATGAT 953
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 954 ATTATCCACACTCTACCCATGCGACTGCAAACTGCAACGCTGCTTACGACGAAACACGA 1013
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheThrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTACCATTCCT 1073
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGCTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1133
 QY 281 HisGluAlaThrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 1134 CATGAGCTTACATGCTTCTGACCATGATGATGATGATGATGATGATGATGATGATGAT 1193
 QY 301 LeuThrValAlaValSerAspAsnProGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 1194 CTATATGT 1253
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerThrSerAsnPro 337
 DB 1254 GTAAACGGGAACTTGACCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 1304

RESULT 15
 AX147840 1020 bp DNA linear PAT 08-JUN-2001
 LOCUS AX147840
 DEFINITION Sequence 85 from Patent W00136473.
 ACCESSION AX147840
 VERSION AX147840.1 GI:14346841
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1020)
 AUTHORS Vogel, J.G., Wood, J.S., Parodi, L.A., Hiesbach, R.R., Lind, P.,
 Slighcom, J., Scheil, R.A., Kayes, P.S., Bannigan, C.M., Ruff, V.,
 Sejlitz, T. and Huff, R.M.
 TITLE Novel 9 protein-coupled receptors
 JOURNAL Patent: WO 0136473-A 85 25-MAY-2001;
 PHARMACIA & UPJOHN COMPANY (US)
 FEATURES
 source 1..1020
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 261 a 263 c 190 g 306 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,13e-123 Length: 1020
 Score: 1724.00 Matches: 335
 Percent Similarity: 99.12% Conservative: 2
 Best Local Similarity: 98.53% Mismatches: 0
 Query Match: 97.35% Indels: 3
 DB: 6 Gaps: 0

US-10-023-775b-2 (1-337) x AX147840 (1-1020)
 QY 1 MetAsnGluProLeuAspThrLeuAlaAsnAlaSerAspPheProAspThrAlaAla 20
 DB 4 ATGAATGACCCACTAGACTATTTAGCAATGCTTCTGATTTCCCGCATATGACGCTGT 63
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisThrLeuProValIleThr 40
 DB 64 TTGGAAATATGACATGATGATAAACAATCCACATCAAGATGACACTACTCCCTGTTATTTAT 123
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValAlaIleSerThrThrIlePhe 60
 DB 124 GCCATATCTCTCTGTTGGATTTCCAGCAATGACATGATATATCCACTTACATTTTC 183
 QY 61 LysMetArgProThrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 184 AAAATGACACTTGGAAAGACAGCAACATATATGCTGATACCTGCGCAGACATTCG 243
 QY 81 LeuThrLeuThrSerLeuProPheLeuIleHisThrThrAlaSerGlyLysAsnThrPhe 100
 DB 244 CTGATATCTGACAGCCCTCCCTCTGATTCATCTACTATGCCAGTGGCAAAACGATGC 303
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuThrSerSer 120
 DB 304 TTGGAGATTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
 QY 121 IleLeuPheLeuThrCysPheSerIlePheAlaGlyThrCysValIleIleHisPrometSer 140
 DB 364 ATCCCTCTCTCTACCTGTTTCAGCATCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 423
 QY 141 CysPheSerIleHisIysThrArgCysAlaValAlaCysAlaValAlaIleIle 160
 DB 424 TCCCTTTCATTCACAAAACGCGATGTCAGTTGAGCCCTGCTGTGGTGGATCAT 483
 QY 161 SerLeuValAlaValIlePromethrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 484 TCACGT 543
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleIleStryPyrAsnLeu 200
 DB 544 TCAGCTGTCTGCGACCTACACGATGCGATGATGATGATGATGATGATGATGATGATGAT 603
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysThrThrThr 220
 DB 604 ATTTGAGCTGCAAGTACTTCTGCTCCCTGGATGATGATGATGATGATGATGATGATGAT 663
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 664 ATTATCCACACTTGTACCCATGCGATGCAAACTGCAACGCTGCTTACGACGAAACACGA 723
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheThrValCysPheLeuProPheHisIleLeu 260
 DB 724 AGGCTACCATTCCT 783
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnI 280
 DB 784 AGGCTCATTCAGAGATGCAATCTACGCTGCTTCAATGATGATGATGATGATGATGATGAT 843
 QY 280 LeHisGluAlaThrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeu 299
 DB 844 TCCATGAGAGCTTACATCTTCTTACACCATATATGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
 QY 300 LeuLeuThrValAlaValSerAspAsnProGlnGlnAlaValCysSerThrValArgCys 319
 DB 904 TTACTATATGT 963
 QY 320 LysValSerGlyAsnLeuGluGlnAlaLysLysIleSerThrSerAsnPro 337
 DB 964 AAAGTACCGGAACTTGACCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAAT 1017

Search completed: May 30, 2003, 00:43:40
 Job time: 3192 secs

Human nGPCR4 #2
Human p2X-11-like rec
Human protein SEQ
Human p2X purinoeco
Human protein SEQ
Human nGPCR4 #1.
Human P2X-purinergic
Purinergic receptor
Purinergic receptor
Human P2X purinoeco
Turkey P2X nucleoco
Gene 374 human sect
Human P2Y4 receptor
Human P2Y4 pyrimido
Human G-protein co
Human G-protein co
Human G-protein co
Human P2Y-1-like GPCR
Human G-protein co
Human G-protein co
Cysteinyl leukotri
Human LTD4 receptor
Human novel polypep
Human CysLT2-like
Human CysLT2 GPCR
Human G-protein co
Human LTD4-like G
Human ATP receptor
Human human secret
Human G-protein co
Human orprian G pro
Human G-protein co
Human polypeptide

PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Lowitz KP;

DR WPI; 2001-355616/37.
 DR N-PSDB; AAS07948.

PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -

PS Claim 53; Page 114-115; 160pp; English.

CC The sequence represents a human G-protein coupled receptor (GPCR),
 CC hRUP21. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

CC Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 22; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHYLPVYGGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHYLPVYGGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGEMNIFGDFMCKFRFHFHNLYSS 120
 DB 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGEMNIFGDFMCKFRFHFHNLYSS 120
 QY 121 ILFLCFSTFRYCVIIHPMSCFSIKHTRCAVAVACAVWIIISLVAVIPMTFLTSTNRNR 180
 DB 121 ILFLCFSTFRYCVIIHPMSCFSIKHTRCAVAVACAVWIIISLVAVIPMTFLTSTNRNR 180
 QY 181 SACLDTSSDELNTIKWYLITATTFCLPIVIVLCTTTIHTLHGLQDSCCLKOKAR 240
 DB 181 SACLDTSSDELNTIKWYLITATTFCLPIVIVLCTTTIHTLHGLQDSCCLKOKAR 240
 QY 241 RLTIILLAFYVCFPHILRVIRIESRLSTISCSIEINOIHEAYIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFYVCFPHILRVIRIESRLSTISCSIEINOIHEAYIVSRPLAALNTFGNLL 300
 QY 301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337
 DB 301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337

RESULT 2

ID AAO15399 standard; protein; 337 AA.

XX AAO15399;

DT 27-SEP-2002 (first entry)

XX

DE Human G protein-coupled receptor.

XX Human; gene therapy; G protein-coupled receptor; drug development;
 KW central nervous system disease; endocrine disease; metabolic disease;
 KW cancer; respiratory disease; digestive disease; immune disease;
 KW inflammation; infection; circulatory disease.

OS Homo sapiens.

XX WO200257441-A1.

XX 25-JUL-2002.

XX 17-JAN-2002; 2002WO-JP00270.

XX 18-JAN-2001; 2001JP-0010714.

XX 30-MAR-2001; 2001JP-0102484.

XX (TAKEDA) TAKEDA CHEM IND LTD.

XX Miwa M, Ito T, Shintani Y, Miyajima N;

DR WPI; 2002-566800/60.

DR N-PSDB; AAL43942.

PT Human kidney-originated G protein-coupled receptor protein TGR30 and
 PT encoded DNA, for developing drugs to treat central nervous diseases,
 PT endocrine diseases, metabolic diseases and cancer, including gene
 PT therapy

PS Claim 1; Page 88-90; 98pp; Japanese.

CC The invention comprises the amino acid and coding sequence of a human G
 CC protein-coupled receptor. The DNA and protein sequences of the invention
 CC are useful for developing drugs to prevent or treat (gene therapy):
 CC central nervous system diseases; endocrine diseases; metabolic diseases;
 CC cancer; respiratory diseases; digestive diseases; immune diseases;
 CC inflammations; infections; and circulatory diseases. The present amino
 CC acid sequence represents the human G protein-coupled receptor of the
 CC invention.

CC Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 23; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHYLPVYGGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHYLPVYGGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGEMNIFGDFMCKFRFHFHNLYSS 120
 DB 61 KMRPKSSTIIMLNACTDLYLTSPLFIHYASGEMNIFGDFMCKFRFHFHNLYSS 120
 QY 121 ILFLCFSTFRYCVIIHPMSCFSIKHTRCAVAVACAVWIIISLVAVIPMTFLTSTNRNR 180
 DB 121 ILFLCFSTFRYCVIIHPMSCFSIKHTRCAVAVACAVWIIISLVAVIPMTFLTSTNRNR 180
 QY 181 SACLDTSSDELNTIKWYLITATTFCLPIVIVLCTTTIHTLHGLQDSCCLKOKAR 240
 DB 181 SACLDTSSDELNTIKWYLITATTFCLPIVIVLCTTTIHTLHGLQDSCCLKOKAR 240
 QY 241 RLTIILLAFYVCFPHILRVIRIESRLSTISCSIEINOIHEAYIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFYVCFPHILRVIRIESRLSTISCSIEINOIHEAYIVSRPLAALNTFGNLL 300
 QY 301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337
 DB 301 LYVVVSDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337

RESULT 3

ABB81902
ID ABB81902 standard; Protein: 337 AA.
XX
AC ABB81902;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human G-protein coupled receptor PFI-019.
XX
KW Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
KW anti-inflammatory; cytosolic; cardiovascular; anti-allergic; hypotensive;
KW anti-atherosclerotic; osteopathic; hypertension; asthma;
KW atherosclerosis.
XX
OS Homo sapiens.
XX
EN EPI219638-A2.
XX
PD 03-JUL-2002.
XX
PE 04-DEC-2001; 2001EP-0310136.
XX
PR 18-DEC-2000; 2000GB-0030854.
XX
PR 04-MAY-2001; 2001GB-0011031.
XX
PA (PFI2) PFIZER LTD.
XX (PFI2) PFIZER INC.
XX
PI Fidoack MD;
XX
XX WPI: 2002-521945/56.
DR N-PSDB: ABQ78847.
XX
PT New G-protein coupled receptor (GPCR) polypeptide with homology to P2Y
PT purinoreceptor, useful for treating e.g. inflammation or cancers in a
PT patient, or for screening GPCR agonists or antagonists for treating
PT these diseases
XX
XX Claim 11; Fig 2; 19pp; English.
XX
XX The invention relates to a novel G-protein coupled receptor (GPCR), and
XX the polynucleotide encoding it. The protein of the invention has
XX neuroprotective, anti-inflammatory, cytosolic, cardiovascular,
XX anti-allergic, hypotensive, anti-atherosclerotic, and osteopathic
XX activity. The GPCR polypeptide is useful for manufacturing a medicament
XX for treating a patient who needs to upregulate a receptor. Preferably,
XX therapeutically useful areas are hypertension, asthma, and
XX atherosclerosis. The sequence represents the G-protein coupled receptor
XX of the invention, PFI-019.
XX
SQ Sequence 337 AA;
Query Match 100.0%; Score 1771; DB 23; Length 337;
Best Local Similarity 100.0%; Pred. No. 2,4e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 RTTLLLAFFVCLPFIHLAVIRIESRLISCSISIQHIAIVSRPLAALMTFGULL 300
QY 301 LYYVSDNFQAVCSIVACKVSGNLEQAKKISYSNNP 337
DB 301 LYYVSDNFQAVCSIVACKVSGNLEQAKKISYSNNP 337
RESULT 4
ID ABB83819 standard; Protein: 337 AA.
XX
AC ABB83819;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human P2Y-1like receptor variant SEQ ID NO 4.
XX
KW Human; P2Y-1like receptor; HIPHUM 0000037; immunity; inflammation;
KW cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
KW immunomodulator; anti-inflammatory; cytosolic; anti-asthmatic;
KW gastrointestinal; anti-ulcer; anti-rheumatic; antiarthritic; virucide;
KW antibacterial; immunosuppressive; dermatological; nephrotropic;
KW anti-allergic; analgesic; receptor.
XX
XX Homo sapiens.
XX
XX GB2369364-A.
XX
XX 29-MAY-2002.
XX
XX 31-AUG-2001; 2001GB-0021215.
XX
XX 01-SEP-2000; 2000GB-0021524.
XX
XX 06-SEP-2000; 2000GB-0021894.
XX
XX 25-SEP-2000; 2000GB-0023444.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Food SM, Ignar DM;
XX
XX WPI: 2002-511268/55.
DR N-PSDB: ABN85630.
XX
PT An isolated P2Y-1like receptor polypeptide (HIPHUM 0000037) which can be
PT used for the identification of agonists and antagonists which may be
PT used to treat an immune or inflammatory disease -
XX
XX Claim 1; Page 30-31; 35pp; English.
XX
XX The invention relates to an isolated P2Y-1like receptor polypeptide
XX (ABB83819-ABB83819) which is also referred to in the specification as
XX HIPHUM 0000037. An effective amount of a substance (agonist or
XX antagonist) which modulates P2Y receptor activity is useful to treat a
XX subject having a disorder that is responsive to P2Y-1like receptor
XX modulation. The disorder is a disease of immunity or inflammation. The
XX substance may also be used to manufacture a medicine for the treatment or
XX prophylaxis of a disorder that is responsive to stimulation or modulation
XX of P2Y-1like receptor activity. Disorders which may be treated include
XX colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
XX gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
XX colitis, rheumatoid arthritis, viral diseases, bacterial infections,
XX autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
XX rhinitis, inflammatory pain and general inflammation such as tendonitis,
XX polymyositis or prostatitis. The invention provides alternative
XX substances for the treatment of immunological and inflammatory diseases.
XX
SQ Sequence 337 AA;
Query Match 100.0%; Score 1771; DB 23; Length 337;
Best Local Similarity 100.0%; Pred. No. 2,4e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNEPDLNANASDPDYAAAFGNCNDENIPKMHYLPVYIGIIFLVGPGNAVISTYLE 60
DB 1 MNEPDLNANASDPDYAAAFGNCNDENIPKMHYLPVYIGIIFLVGPGNAVISTYLE 60
QY 61 KMRPKSSTIIMNACTDLVLTSLPFLIHYASGEMNIFGDMCKFRFSFHNLYSS 120
DB 61 KMRPKSSTIIMNACTDLVLTSLPFLIHYASGEMNIFGDMCKFRFSFHNLYSS 120
QY 121 IFLFCFSIFRCVCIHHPMSCFSIHKTRCAVACAAVWIIISLVAVIPMFLISTNRTNR 180
DB 121 IFLFCFSIFRCVCIHHPMSCFSIHKTRCAVACAAVWIIISLVAVIPMFLISTNRTNR 180
QY 181 SACLDITSSDELNTIKWMLITATFTCLPLVIVTLCYTTIIHTLTHGLQDTSCLKOKAR 240
DB 181 SACLDITSSDELNTIKWMLITATFTCLPLVIVTLCYTTIIHTLTHGLQDTSCLKOKAR 240
QY 241 RLTIILLAFVYCFEPFLILRVIRISRLISCSISENOIHEAVIYSRPLAALNFTGNLL 300
DB 241 RLTIILLAFVYCFEPFLILRVIRISRLISCSISENOIHEAVIYSRPLAALNFTGNLL 300
QY 301 LYVVSDFNQAVCSFVRCKVSGNLEQAKKISYSNNP 337
DB 301 LYVVSDFNQAVCSFVRCKVSGNLEQAKKISYSNNP 337

RESULT 5
AAE21803
ID AAE21803 standard; Protein; 337 AA.
AC AAE21803;
XX
XX
DT 16-JUL-2002 (first entry)
DE Human AXOR89 (G-protein coupled receptor) protein.
XX
XX
KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
KW infection; cancer; pain; asthma; Parkinson's Disease; diabetes; obesity;
KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;
KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
KW myocardial infarction; allergy; benign prostatic hypertrophy; migraine;
KW vomiting; psychotic; neurological disorder; anxiety; manic depression;
KW delirium; Huntington's Disease; Gilles de la Tourette's syndrome;
KW dementia; dyskinesia.
XX
XX
OS Homo sapiens.
XX
XX
PN GB2365012-A.
XX
XX
PD 13-FEB-2002.
XX
XX
PF 10-MAY-2001; 2001GB-0011437.
XX
XX
XX 11-MAY-2000; 2000US-0569137.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX (SMK ) SMITHKLINE BEECHAM PLC.
XX
XX Elshourbagy N, Shabon U;
XX
XX WPI: 2002-332558/37.
XX N-PSDB; AAD34278.
XX
XX Novel AXOR89 polypeptide and polynucleotide encoding it, useful for
XX identifying agonists and antagonists in the treatment of diseases
XX associated with an AXOR89 imbalance, such as cancers, diabetes or
XX asthma -
XX
XX Claim 1; Page 30; 37pp; English.
XX
XX The invention relates to an isolated AXOR89 polypeptide (G-protein
XX coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
XX and polynucleotide encoding the polypeptide, is useful for identifying
XX agonists and antagonists (or inhibitors) that are potentially useful in

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CC treating conditions associated with an AXOR89 imbalance, such as
CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart
CC failure, hypotension, hypertension, urinary retention, osteoporosis,
CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
CC syndrome. The polynucleotide sequence may also be used for chromosome
CC localisation or tissue expression studies. The AXOR89 is used as a
CC vaccine or to produce fusion proteins. The present sequence is human
CC AXOR89 protein.
XX
XX
SQ Sequence 337 AA;
XX
Query Match 100.0%; Score 1771; DB 23; Length 337;
Best Local Similarity 100.0%; Pred. No. 2,4e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPDLNANASDPDYAAAFGNCNDENIPKMHYLPVYIGIIFLVGPGNAVISTYLE 60
DB 1 MNEPDLNANASDPDYAAAFGNCNDENIPKMHYLPVYIGIIFLVGPGNAVISTYLE 60
QY 61 KMRPKSSTIIMNACTDLVLTSLPFLIHYASGEMNIFGDMCKFRFSFHNLYSS 120
DB 61 KMRPKSSTIIMNACTDLVLTSLPFLIHYASGEMNIFGDMCKFRFSFHNLYSS 120
QY 121 IFLFCFSIFRCVCIHHPMSCFSIHKTRCAVACAAVWIIISLVAVIPMFLISTNRTNR 180
DB 121 IFLFCFSIFRCVCIHHPMSCFSIHKTRCAVACAAVWIIISLVAVIPMFLISTNRTNR 180
QY 181 SACLDITSSDELNTIKWMLITATFTCLPLVIVTLCYTTIIHTLTHGLQDTSCLKOKAR 240
DB 181 SACLDITSSDELNTIKWMLITATFTCLPLVIVTLCYTTIIHTLTHGLQDTSCLKOKAR 240
QY 241 RLTIILLAFVYCFEPFLILRVIRISRLISCSISENOIHEAVIYSRPLAALNFTGNLL 300
DB 241 RLTIILLAFVYCFEPFLILRVIRISRLISCSISENOIHEAVIYSRPLAALNFTGNLL 300
QY 301 LYVVSDFNQAVCSFVRCKVSGNLEQAKKISYSNNP 337
DB 301 LYVVSDFNQAVCSFVRCKVSGNLEQAKKISYSNNP 337

RESULT 6
ABB79438
ID ABB79438 standard; Protein; 337 AA.
AC ABB79438;
XX
XX
DT 05-JUL-2002 (first entry)
DE Human P2Y1-11.
XX
XX
XX Human; P2Y1-11; G protein-coupled; receptor; gene therapy; thyroid.
XX
XX
XX Homo sapiens.
XX
XX
XX DE10046970-A1.
XX
XX PD 11-APR-2002.
XX
XX PF 22-SEP-2000; 2000DE-1046970.
XX
XX PR 22-SEP-2000; 2000DE-1046970.
XX
XX (BRUE/) BRUESS M.
XX (BOEN/) BOENISCH H.
XX
XX Bruess M, Boenisch H;
XX
XX WPI: 2002-353329/39.
XX N-PSDB; ABL56197.

```

XX New human P2Y11 gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 XX
 PS Claim 4; Page 3; 5pp; German.
 XX
 CC The invention relates to the human P2Y11 gene (1), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (1) and related mRNA, cDNA, protein, antibodies
 CC etc., are used for diagnosis and (gene) therapy of diseases that are
 CC (in)directly associated with (1) or its expression products. No diseases
 CC are specified but as (1) is expressed only in thyroid tissue, (1) is
 CC presumed to be involved in regulation of thyroid function. The present
 CC sequence is that of P2Y11.
 CC
 XX Sequence 337 AA:
 Q
 Query Match 100.0%; Score 1771; DB 23; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIF 60
 DB 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIF 60
 QY 61 KMPPKSSSTIMLNACTDLYLTSPLFIHYASGENMIFGDMCKFIKFSHFNLSS 120
 DB 61 KMPPKSSSTIMLNACTDLYLTSPLFIHYASGENMIFGDMCKFIKFSHFNLSS 120
 QY 121 ILFLTCSIFRYCVIIHPMCSFISIKTRCAVAVCAVWIIISLVAVIPMTFLISTNTNR 180
 DB 121 ILFLTCSIFRYCVIIHPMCSFISIKTRCAVAVCAVWIIISLVAVIPMTFLISTNTNR 180
 QY 181 SACLDTSSDELMTIKWNYLILATATPCPLVIVTLCYTTIHTLHGLTDSCLKOKAR 240
 DB 181 SACLDTSSDELMTIKWNYLILATATPCPLVIVTLCYTTIHTLHGLTDSCLKOKAR 240
 QY 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFGNL 300
 DB 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFGNL 300
 QY 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISYNNP 337
 DB 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISYNNP 337
 b
 RESULT 7
 AAU77600 standard; Protein; 337 AA.
 ID AAU77600:
 AC AAU77600:
 DT 05-JUN-2002 (first entry)
 XX
 DE Human P2Y1-like G protein-coupled receptor.
 XX
 KW Human: P2Y1-like G protein-coupled; receptor; GPCR;
 KW Infection; pain; cancer; anorexia; bulimia; asthma; hypotension;
 KW central nervous system disease; acute heart failure; hypertension;
 KW urinary retention; osteoporosis; diabetes; angina pectoris;
 KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 KW benign prostatic hypertrophy; psychosis; neurological disorder;
 KW dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
 KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 KW dementia; severe mental retardation; Huntington's disease;
 KW Tourette's syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200214511-A2.
 XX
 PD 21-FEB-2002.

XX
 PF 10-AUG-2001; 2001WO-EP09243.
 XX
 PR 14-AUG-2000; 2000US-224989P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI, 2002-257607/30.
 XX
 DR N-PSDB; ABK11381.
 PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can
 PT be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 CC
 PS Claim 25; Fig 2; 118pp; English.
 XX
 CC The invention relates to a purified human P2Y1-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y1-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention, ulcer,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence represents the P2Y1-like GPCR of the invention.
 CC
 XX Sequence 337 AA:
 QY
 Query Match 100.0%; Score 1771; DB 23; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIF 60
 DB 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIF 60
 QY 61 KMPPKSSSTIMLNACTDLYLTSPLFIHYASGENMIFGDMCKFIKFSHFNLSS 120
 DB 61 KMPPKSSSTIMLNACTDLYLTSPLFIHYASGENMIFGDMCKFIKFSHFNLSS 120
 QY 121 ILFLTCSIFRYCVIIHPMCSFISIKTRCAVAVCAVWIIISLVAVIPMTFLISTNTNR 180
 DB 121 ILFLTCSIFRYCVIIHPMCSFISIKTRCAVAVCAVWIIISLVAVIPMTFLISTNTNR 180
 QY 181 SACLDTSSDELMTIKWNYLILATATPCPLVIVTLCYTTIHTLHGLTDSCLKOKAR 240
 DB 181 SACLDTSSDELMTIKWNYLILATATPCPLVIVTLCYTTIHTLHGLTDSCLKOKAR 240
 QY 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFGNL 300
 DB 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFGNL 300
 QY 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISYNNP 337
 DB 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISYNNP 337
 RESULT 8

AA014027
ID AA014027 standard; Protein: 337 AA.
AC AA014027;
XX
XX
DT 30-APR-2002 (first entry)
XX
XX Human purinergic-related G-protein coupled receptor (GPCR).
DE
XX
XX Human: chromosome 13; purinergic GPCR; G-protein coupled receptor;
KW signal transduction; human: protease; GPCR disorder; gene therapy;
KW transgenic animal; receptor.
XX
XX Homo sapiens.
OS
XX
XX MO200187980-A2.
PN
XX
XX 22-NOV-2001.
PD
XX
XX 17-MAY-2001; 2001WO-US15957.
PF
XX
XX 18-MAY-2000; 2000US-205196P.
PR 08-AUG-2000; 2000US-0634656.
XX
XX (APPL-) APPLERA CORP.
XX
XX Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
PI
XX
XX WPI: 2002-075312/10.
DR N-PSDB: AAK98323, AAK98324.
XX
XX Novel isolated G-protein coupled receptor peptide useful for treating
PT disorder characterised by absence of, in appropriate or unwanted
PT expression of the receptor protein, and as immunogens to raise
PT antibodies -
XX
XX Claim 1; Fig 2; 64pp; English.
XX
XX The present specifically claimed sequence represents a human
PS purinergic-related G-protein coupled receptor (GPCR) encoded by a gene on
XX chromosome 13. GPCRs constitute a major class of proteins responsible for
XX signal transduction within a cell. Upon binding of a ligand to the
XX extracellular portion of a GPCR, a signal is transduced resulting in a
XX biological or physiological change within the cell. The GPCR proteins can
XX be divided into five families, family I contains the purinergic GPCRs
XX (e.g. the P2Y receptors). P2Y receptors are characterised by their
XX selective responsiveness towards ATP and its analogues, some also respond
XX to UTP. The invention comprises a human G-protein coupled receptor
XX protein and encoding nucleic acids. The GPCR protein and nucleic acids of
XX the invention are useful in the treatment of a disease or condition
XX mediated by a human protease. The GPCR protein of the invention is useful
XX for: the development/identification of therapeutic proteins; assays
XX designed to quantitatively determine levels of the protein in biological
XX fluids; identifying compounds which modulate the activity of the GPCR, or
XX the interaction of the GPCR and a molecule with which it normally
XX interacts; and treating a disorder characterised by an absence of, or
XX inappropriate expression of the GPCR protein. The GPCR nucleic acids of
XX the invention are useful in diagnostic assays to identify changes in the
XX GPCR nucleic acid that lead to pathology; controlling GPCR expression;
XX and in gene therapy to treat patients with aberrant GPCR gene expression.
XX The GPCR nucleic acids can also be used in the production of transgenic
XX animals.
XX
XX Sequence 337 AA:
SQ

Query Match 100.0%; Score 1771; DB 23; Length 337;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPILDYLANASDPDYAAAFGNCNDENTPLKMHYLPVYGIIFVGFPGNVMVISTYF 60
DB 1 MNEPILDYLANASDPDYAAAFGNCNDENTPLKMHYLPVYGIIFVGFPGNVMVISTYF 60

QY 61 KMRPKSSSTIIMNLACTDLYLTSLPFLIHVYASGEMNIFGDMCKEIRFSFHNLYSS 120
DB 61 KMRPKSSSTIIMNLACTDLYLTSLPFLIHVYASGEMNIFGDMCKEIRFSFHNLYSS 120
QY 121 ILFLTCFSIFRCVILIHPSGCSHKTRCAVAVACAWMISLVANVIMPTFLTSTNRNR 180
DB 121 ILFLTCFSIFRCVILIHPSGCSHKTRCAVAVACAWMISLVANVIMPTFLTSTNRNR 180
QY 181 SACLDTSSDELNTKMYNLITATTFCLPLVIVLCTTIHTLTHGLQDSCIKOKAR 240
DB 181 SACLDTSSDELNTKMYNLITATTFCLPLVIVLCTTIHTLTHGLQDSCIKOKAR 240
QY 241 RLTIILLAFYVCFPLPHILRVIRIESRLSISCSIEHQIHEAVYVSREPLALNTEGNL 300
DB 241 RLTIILLAFYVCFPLPHILRVIRIESRLSISCSIEHQIHEAVYVSREPLALNTEGNL 300
QY 301 LYVVVSDNFQOAVGCTVRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVVSDNFQOAVGCTVRCKVSGNLEQAKKISYNNP 337

RESULT 9
ID AAE16171 standard; Protein: 337 AA.
AC AAE16171;
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human G-protein coupled receptor 2 (GCR2-2) protein.
DE
XX
XX Human; G-protein coupled receptor 2; cell proliferative disorder;
KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
KW gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
KW acquired immune deficiency syndrome; inflammatory disorder; infection;
KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
KW diabetes; obesity; osteoporosis; gene therapy; GCR2-2.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 35..59 /note="Transmembrane domain"
FT
XX
XX MO200187937-A2.
XX
XX 22-NOV-2001.
PD
XX
XX 17-MAY-2001; 2001WO-US16285.
PF
XX
XX 18-MAY-2000; 2000US-205628P.
PR 22-MAY-2000; 2000US-206222P.
XX 25-MAY-2000; 2000US-207566P.
PR 02-JUN-2000; 2000US-208834P.
XX 02-JUN-2000; 2000US-208861P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Patterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R;
PI Khan FA, Gandhi AR, Walla NK, Nguyen DB, Yue H, Hafalia A;
PI Elliott VS, Lal P, Reddy R, Kallilick DA, Tang TY, Au-Young J;
XX
XX WPI: 2002-089844/12.
DR N-PSDB: AAD26370.
XX
XX Novel G-protein coupled receptors and polynucleotides useful for
PT diagnosis, treatment and prevention of disorders of cell proliferation,
PT neurological, cardiovascular, metabolic disorders and viral infections
PT
XX
XX Claim 1; Page 104-105; 115pp; English.

XX The invention relates to human G-protein coupled receptor (GPRC)
 CC polypeptides and polynucleotides. GPRC polypeptides are useful for
 CC screening compounds that modulate their activity. They are useful in
 CC the diagnosis, prevention and treatment of disorders which include
 CC cell proliferative disorders such as arteriosclerosis, hepatitis,
 CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
 CC lymphoma; neurological disorders such as epilepsy, ischaemic
 CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
 CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
 CC meningitis, Creutzfeldt-Jakob disease, schizophrenia disorders, amnesia;
 CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
 CC hypertension, vascular tumours, myocardial infarction, hypertensive
 CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;
 CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,
 CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
 CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
 CC encephalopathy, autoimmune/inflammatory disorders such as Addison's
 CC disease, allergies, sporidylitis, amyloidosis, anaemia, asthma, contact
 CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
 CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
 CC fungal, parasitic, protozoal and helminthic infections and trauma;
 CC metabolic disorders such as diabetes, obesity and osteoporosis; and
 CC viral infections such as infection caused by viral agent classified as
 CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention
 CC are useful as probes for assessing toxicity of test compounds. They are
 CC also used in gene therapy. The present sequence is human G-protein
 CC coupled receptor 2 (GPRC-2) protein.

XX Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 23; Length 337;

Best Local Similarity 100.0%; Pred. No. 2.4e-194; Mismatches 0; Indels 0; Gaps 0;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAFGNCNDENIPKMHYLPYIGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPLDYLANASDFPDYAAFGNCNDENIPKMHYLPYIGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKSSTIIMLNACTDLYLTLSPPLIHYYAGSEWIMIGDFCKRIRSFHNLYSS 120
 DB 61 KMRPKSSTIIMLNACTDLYLTLSPPLIHYYAGSEWIMIGDFCKRIRSFHNLYSS 120
 Y 121 ILFLTCSIFRCVCIHHMSEFSTHKTRCAVAVACAVWVITSLVAVIPMTFLTSTNRTNR 180
 DB 121 ILFLTCSIFRCVCIHHMSEFSTHKTRCAVAVACAVWVITSLVAVIPMTFLTSTNRTNR 180
 QY 181 SACLDUTSSDELNTKYNLITATTPCLPIVIVLCYTTIHTHTHGLQDSCCKOKAR 240
 DB 181 SACLDUTSSDELNTKYNLITATTPCLPIVIVLCYTTIHTHTHGLQDSCCKOKAR 240
 QY 241 RLTILLALAFYVCFPHILNVRIRISRLISCSIEINOIHNAVIVSRPLAINTFGNLT 300
 DB 241 RLTILLALAFYVCFPHILNVRIRISRLISCSIEINOIHNAVIVSRPLAINTFGNLT 300
 QY 301 LYVVSDFNQAVGCTVRCKYSGNLEQAKKISYSNNP 337
 DB 301 LYVVSDFNQAVGCTVRCKYSGNLEQAKKISYSNNP 337

RESULT 10

ID AAU04584 standard; Protein; 337 AA.

XX AAU04584;

DT 26-SEP-2001 (first entry)

XX Human G-protein coupled receptor, GPCR 39404.

KM Human; G-protein coupled receptor; GPCR; 39404; Immunogen; antibody;

KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;

KM Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
 KW systemic lupus erythematosus; actinic keratosis; myocarditis;
 KW Kawasaki syndrome; Digorge syndrome; peripheral B-cell neoplasm;
 KW inflammations; teratoma.

OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 116..126
 /label= Biologically-active_peptide

PN WO200149847-A2;

PD 12-JUL-2001.

PF 22-DEC-2000; 2000MO-US35309.

PR 30-DEC-1999; 99US-0475790.

PA (MILL-) MILLENNIUM PHARM INC.

PI Glucksmann MA, White D;

DR WPI; 2001-432880/46.

DR N-PSDB; AAS08362.

PT Novel isolated 26904, 38911 and 39404 polypeptides which are seven
 PT transmembrane proteins belonging to superfamily of G-protein-coupled
 PT receptors, useful for treating disorders of spleen, lung, liver, brain
 and kidney -

PS Claim 8; Fig 1; 164pp; English.

The sequence represents a novel human seven transmembrane domain
 CC protein belonging to the G-protein coupled receptor (GPCR) superfamily,
 CC protein 39404. The receptor is useful in drug screening assays, to
 CC identify compounds that modulate receptor activity and/or interact with
 CC the receptor, and for producing antibodies specific for the receptor, its
 CC regions or fragments. The receptor is useful for treating/diagnosing a
 CC 26904, 38911 and 39404 protein-associated disorder characterised by
 CC aberrant expression or activity of the protein, for monitoring
 CC the therapeutic effect during clinical trials and other treatment, as bait
 CC proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
 CC analysis. The protein and nucleic acids encoding them are useful for
 CC diagnosis and treatment of disorders selected from disorders of the
 CC spleen, lung such as Good pasture's syndrome, liver such as viral
 CC hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
 CC such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
 CC disease, colon such as Crohn's disease, uterus and endometrium such as
 CC endometriosis, T-cell disorders such as systemic lupus erythematosus,
 CC diseases of the skin such as actinic keratosis, disorders of the heart
 CC such as myocarditis, disorders involving blood vessels such as Kawasaki
 CC syndrome, disorders involving the thymus such as Digorge syndrome,
 CC disorders involving B-cells such as peripheral B-cell neoplasms,
 CC disorders of the breast such as inflammations, and disorders involving
 CC the testis and epididymis such as teratoma. Numerous examples of
 CC each type of disorder are given in the specification.

SO Sequence 337 AA;

Query Match 99.6%; Score 1764; DB 22; Length 337;

Best Local Similarity 99.7%; Pred. No. 1.5e-193; Mismatches 1; Indels 0; Gaps 0;

Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNEPLDYLANASDFPDYAAFGNCNDENIPKMHYLPYIGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPLDYLANASDFPDYAAFGNCNDENIPKMHYLPYIGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKSSTIIMLNACTDLYLTLSPPLIHYYAGSEWIMIGDFCKRIRSFHNLYSS 120
 DB 61 KMRPKSSTIIMLNACTDLYLTLSPPLIHYYAGSEWIMIGDFCKRIRSFHNLYSS 120
 QY 121 ILFLTCSIFRCVCIHHMSEFSTHKTRCAVAVACAVWVITSLVAVIPMTFLTSTNRTNR 180


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Db      121 IIFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLTSTNRTNR 180
Oy      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTIHTLTHGLOTDSCLOKAR 240
Db      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTIHTLTHGLOTDSCLOKAR 240
Oy      241 RTIILLAFYVCFELPHILRVIRIESRLSISCSISINOIHEAVIYSRPLAALNTFENL 300
Db      241 RTIILLAFYVCFELPHILRVIRIESRLSISCSISINOIHEAVIYSRPLAALNTFENL 300
Oy      301 LYYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSNP 337
Db      301 LYYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSNP 337

RESULT 11
AAG80971
ID      AAG80971 standard; Protein; 336 AA.
AC      AAG80971;
XX      28-AUG-2001 (first entry)
DT      Human nGPRC54 #2.
XX      G protein-coupled receptor; nGPRC; seven transmembrane receptor;
KM      signal transduction; schizophrenia; thyroid disorder; renal failure;
KM      rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KM      cardiovascular disease; proliferative disorder; hormonal disorder;
KM      neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KM      attention deficit-hyperactivity disorder; attention deficit disorder;
KM      Parkinson's disease; migraine; senile dementia; inflammatory disease;
KM      rheumatoid arthritis; autoimmune disorder; respiratory ailment;
XX      neuroprotective.
OS      Homo sapiens.
XX      WO200136473-A2.
XX      25-MAY-2001.
XX      16-NOV-2000; 2000MO-US31581.
XX      16-NOV-1999; 9905-0165838.
XX      17-NOV-1999; 9905-0166071.
XX      19-NOV-1999; 9905-0166678.
XX      28-DEC-1999; 9905-0173396.
XX      22-FEB-2000; 2000US-0184129.
XX      28-FEB-2000; 2000US-0185421.
XX      28-FEB-2000; 2000US-0185554.
XX      02-MAR-2000; 2000US-0186530.
XX      03-MAR-2000; 2000US-0186811.
XX      09-MAR-2000; 2000US-0188114.
XX      17-MAR-2000; 2000US-0190310.
XX      21-MAR-2000; 2000US-0190800.
XX      20-APR-2000; 2000US-0198568.
XX      02-MAY-2000; 2000US-0201190.
XX      08-MAY-2000; 2000US-0203111.
XX      25-MAY-2000; 2000US-0207094.
XX      (PHAA ) PHARMACIA & UPJOHN CO.
XX      Vogeli G , Wood LS, Parodi LA, Hiesch RR, Lind P, Slightom J;
PI      Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Ruff RM;
XX      WPI; 2001-389626/41.
XX      N-PSDB; AAH51011.
XX      New G protein-coupled receptor (nGPRC-x) and its encoding
PT      polynucleotide useful for diagnosing and treating e.g. schizophrenia
XX      Claim 37; Page 91; 261pp; English.

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XX      The present invention relates to novel G protein-coupled receptors
CC      (nGPRC; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
CC      28, 31-38, 40, 41, 53-60) and their coding sequences. The present
CC      sequence is one such G protein-coupled receptor. GPRs are also known as
CC      seven transmembrane receptors and function in signal transduction. The
CC      nGPRC coding sequences are useful for screening a human to diagnose a
CC      disorder affecting the brain or a genetic predisposition, specifically
CC      schizophrenia. nGPRC are useful for identifying compounds useful for
CC      treating schizophrenia. Detection of nGPRC in a sample is useful as a
CC      diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC      failure, rheumatoid arthritis, CNS disorders, infectious such as HIV-1,
CC      metabolic and cardiovascular diseases, proliferative disorders and
CC      hormonal disorders. Modulators of nGPRC activity have the utility for
CC      treating neurological disorders, including schizophrenia, ADHD/ADD
CC      (attention deficit-hyperactivity disorder/attention deficit disorder),
CC      and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC      migraine and senile dementia. Additional disorders include inflammatory
CC      conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC      disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC      diseases e.g.. inflammatory bowel disease.
XX      Sequence 336 AA:
SQ      Query Match 90.5%; Score 1602.5; DB 22; Length 336;
        Best Local Similarity 92.0%; Pred. No. 5.1e-175;
        Matches 312; Conservative 6; Mismatches 14; Indels 7; Gaps 3;
Oy      1 MNEPDLVLANASPPRYAAAFGCTDENTIPKHHYIPVYIGTIFLVGPGNAVISTYTF 60
Db      1 MNEPDLVLANASPPRYAAAFGCTDENTIPKHHYIPVYIGTIFLVGPGNAVISTYTF 60
Oy      61 KMRPKSSTIIMNLACTDLTYTSLPFLIHYVASEGNTFQPMKFTFESHFNYLSS 120
Db      61 KMRPKSSTIIMNLACTDLTYTSLPFLIHYVASEGNTFQPMKFTFESHFNYLSS 120
Oy      121 IIFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLTSTNRTNR 180
Db      121 IIFLTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLTSTNRTNR 180
Oy      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTIHTLTHGLOTDSCLOKAR 240
Db      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTIHTLTHGLOTDSCLOKAR 240
Oy      241 RTIILLAFYVCFELPHILRVIRIESRLSISCSISINOIHEAVIYSRPLAALNTF 296
Db      241 RTIILLAFYVCFELPHILRVIRIESRLSISCSISINOIHEAVIYSRPLAALNTF 296
Oy      297 GNILLVYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSN 335
Db      297 GNILLVYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSN 336

RESULT 12
ABB83818
ID      ABB83818 standard; Protein; 276 AA.
AC      ABB83818;
XX      18-SEP-2002 (first entry)
DT      Human P2Y-1like receptor SEQ ID NO. 2.
XX      Human P2Y-1like receptor SEQ ID NO. 2.
DE      Human: P2Y-1like receptor; HIPHM 0000037; immunity; inflammation;
XX      cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
KM      immunomodulator; anti-inflammatory; cytoskeletal; antisthmatic;
KM      gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virocidic;
KM      antibacterial; immunosuppressive; dermatological; nephrotropic;
XX      antiallergic; analgesic; receptor.
OS      Homo sapiens.
XX      GB2369364-A.

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XX 29-MAY-2002.
PD 31-AUG-2001; 2001GB-0021215.
XX
XX
XX 01-SEP-2000; 2000GB-0021524.
XX 06-SEP-2000; 2000GB-0021894.
PR 25-SEP-2000; 2000GB-0023444.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Foord SM, Ignar DM;
XX
XX MPI: 2002-511268/55.
DR N-PSDB; ABR85629.
XX
XX An isolated p2y-1like receptor polypeptide (HIPHUM 0000037) which can be
PT used for the identification of agonists and antagonists which may be
PT used to treat an immune or inflammatory disease -
XX
XX Claim 1; Page 27-28; 35pp; English.
XX
XX The invention relates to an isolated p2y-1like receptor polypeptide
CC (ABR83818-ABR83819) which is also referred to in the specification as
CC HIPHUM 0000037. An effective amount of a substance (agonist or
CC antagonist) which modulates p2y receptor activity is useful to treat a
CC subject having a disorder that is responsive to p2y-1like receptor
CC modulation. The disorder is a disease of immunity or inflammation. The
CC substance may also be used to manufacture a medicine for the treatment or
CC prophylaxis of a disorder that is responsive to stimulation or modulation
CC of p2y-1like receptor activity. Disorders which may be treated include
CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
CC polymyositis or prostatitis. The invention provides alternative
CC substances for the treatment of immunological and inflammatory diseases.
XX
SQ Sequence 276 AA:
Query Match 81.5%; Score 1444; DB 23; Length 276;
Best Local Similarity 100.0%; Pred. No. 6e-157;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 MRPKSSTIIMLNACTDLTYTSLPFLIHVYASGENWIFGDFMCKFRFSFHNLYSSI 121
DB 1 MRPKSSTIIMLNACTDLTYTSLPFLIHVYASGENWIFGDFMCKFRFSFHNLYSSI 60
QY 122 LFLTGFSTFRVCVLIHSPSCFSIHKTRCAVAVCAVAVIISLVAVIMPTFLTSTNRTRS 181
DB 61 LFLTGFSTFRVCVLIHSPSCFSIHKTRCAVAVCAVAVIISLVAVIMPTFLTSTNRTRS 120
QY 182 ACIDLTSSDELNTIKWYMLITATPCLPLVIVTLCYTTIIHTLTHGQTDSCLEKOKARR 241
DB 121 ACIDLTSSDELNTIKWYMLITATPCLPLVIVTLCYTTIIHTLTHGQTDSCLEKOKARR 180
QY 242 LFTLLLLAFYVCFELPFLHRLVIRIESRLISCSISCTENOIHEAVIYSRPLALNTFGNLL 301
DB 181 LFTLLLLAFYVCFELPFLHRLVIRIESRLISCSISCTENOIHEAVIYSRPLALNTFGNLL 240
QY 302 YVVVSDNQOAVCSIVRCVSGNLQOAKKISYNNP 337
DB 241 YVVVSDNQOAVCSIVRCVSGNLQOAKKISYNNP 276

RESULT 13
AAM79297
ID AAM79297 standard; Protein; 230 AA.
AC AAM79297;
XX
XX 06-NOV-2001 (first entry)
DT

XX
DE Human protein SEQ ID NO 1959.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0634936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX MPI: 2001-476283/51.
XX N-PSDB; AAK52430.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 4370-4371; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 230 AA:
Query Match 62.2%; Score 1102; DB 22; Length 230;
Best Local Similarity 100.0%; Pred. No. 8e-118;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDPDYAAAGNCNDENIPKMHYLPVYIGTIFLVGPGNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAGNCNDENIPKMHYLPVYIGTIFLVGPGNAVISTYIF 60
QY 61 KMRPKSSTIIMLNACTDLTYTSLPFLIHVYASGENWIFGDFMCKFRFSFHNLYSSI 120
DB 61 KMRPKSSTIIMLNACTDLTYTSLPFLIHVYASGENWIFGDFMCKFRFSFHNLYSSI 120
QY 121 ILFTGFSIFRCVLIHSPSCFSIHKTRCAVAVCAVAVIISLVAVIMPTFLTSTNRTR 180
DB 121 ILFTGFSIFRCVLIHSPSCFSIHKTRCAVAVCAVAVIISLVAVIMPTFLTSTNRTR 180
QY 181 SACIDLTSSDELNTIKWYMLITATP 206

Db 181 SACLDTSSDELTKMYNLTRAT 206

|||||

RESULT 14

ABBI1082

ID ABBI1082 standard; peptide; 179 AA.

XX

AC ABBI1082;

XX

DT 11-JAN-2002 (first entry)

XX

DE Human p21 purinoceptor homologue, SEQ ID NO:1452.

XX

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;

KM haematopoiesis regulation; tissue growth; immunomodulator; activin;

KM inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;

KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KM chronic inflammatory condition; proliferative retinopathy;

KM atherosclerosis; coronary heart disease; arterial ischaemia;

KM bone disorder; osteoporosis; vascular growth disorder;

KM tissue regeneration; wound healing; infection; immune disorder;

KM cell culture; drug screening; gene therapy; antiinflammatory;

KM antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;

KM cytosolic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

KM antifungal; vulnery; antiulcer.

XX

OS Homo sapiens.

XX

PN W0200157188-A2.

XX

PD 09-AUG-2001.

XX

PE 05-FEB-2001; 2001WO-US03800.

XX

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

XX

XX (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457740/49.

DR N-PSDB; ABA08326.

XX

PT Human proteins and DNA encoding sequences useful for preventing,

PT treating or ameliorating a medical condition in a mammalian subject

PT e.g. arthritis and cancer -

XX

PS Claim 20; Page 144; 1963pp; English.

XX

XX Sequences ABBI0981-ABBI12330 represent 1350 novel human polypeptides, and

XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

XX invention also relates to vectors and recombinant host cells comprising a

XX nucleotide of the invention, methods of producing the novel polypeptides,

XX antibodies against the polypeptides, methods of detecting the nucleotides

XX or polypeptides in a sample, and methods of identifying compounds which

XX bind to polypeptides of the invention. Although novel, many of the

XX polypeptides of the invention have homology to known proteins, thereby

XX giving an insight into their probable biological activities, and hence

XX potential therapeutic applications. The polypeptides of the invention may

XX have various activities, including cytokine, cell proliferation or cell

XX differentiation activities; stem cell growth factor activity;

XX haematopoiesis regulatory activity; tissue growth activity;

XX immunomodulatory activity; activin- or inhibin-related activities;

XX chemotactic or chemokinetic activities; haemostatic, thrombotic or

XX thrombolytic activities; receptor or ligand activities; or may be

XX involved in oncogenesis, cancer cell proliferation or metastasis.

XX Depending on their biological activities, polypeptides and nucleotides of

XX the invention are useful for preventing, treating or ameliorating medical

XX conditions, e.g., by protein or gene therapy. Such conditions include

XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention.

XX

SO Sequence 179 AA;

Query Match 49.8%; Score 881.5; DB 22; Length 179;

Best Local Similarity 94.9%; Pred. No. 1.1e-92;

Matches 169; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 70 IIMLNACDPLVLTSLPILIHVYASGEMNIFGDFMCKFRFSFHEMLYSIIFLCFSI 129

Db 3 IIMLNALITDPLVLTSLPILIHVYASGEMNIFGDFMCKFRFSFHEMLYSIIFLCFSI 62

OY 130 FRCVITHPMCSFIRHRCACAVACAVWIIISLVAVIPMFLITSTRTRRSACLDITSS 189

Db 63 FRCVITHPMCSFIRHRCACAVACAVWIIISLVAVIPMFLITSTRTRRSACLDITSS 122

OY 190 DELNTIKWYMLITATFCLPLVIVTLCTYTTIHTLTHGILDTSCCLKQKARRITILL 247

Db 123 DELNTIKWYMLITLA-LLCPLVIVTLCTYTTIHTLTHGIANSCCLKQKARRITILL 179

XX

RESULT 15

AAM80281

ID AAM80281 standard; Protein; 179 AA.

XX

AC AAM80281;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human protein seq ID NO 3927.

XX

KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

XX

OS Homo sapiens.

XX

PN W0200157190-A2.

XX

PD 09-AUG-2001.

XX

PE 05-FEB-2001; 2001WO-US04098.

XX

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

XX

XX (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;

PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AD, Yang Y, Wejhtman T, Goodrich R;

XX MPI: 2001-476283/51.
DR N-PSDB; AAK53414.
XX
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
PS
XX Claim 20; Page 470; 6221ip; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haemopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/limbin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAW80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:44:43 ; Search time 21 Seconds
(without alignments)
1624.399 Million cell updates/sec

Title: US-10-023-775b-2
Perfect score: 1771
Sequence: 1 MNEPLDYLANASDPDYAA.....RCKVSGNLBOAKISYNNP 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1771	100.0	337	9	US-10-023-775b-2
2	1771	100.0	337	9	US-10-270-144-2
3	1771	100.0	337	9	US-10-188-405-8
4	1771	100.0	337	9	US-09-885-453-1
5	1771	100.0	337	10	US-09-943-798-4
6	1602.5	90.5	336	9	US-09-782-974C-86
7	1444	81.5	276	10	US-09-943-798-2
8	831.5	47.0	192	9	US-09-782-974C-60
9	575	32.5	299	9	US-10-270-144-4
10	567	32.0	373	9	US-10-092-135-6
11	565.5	31.9	362	9	US-10-092-135-3
12	565.5	31.9	362	9	US-10-092-135-4
13	565.5	31.9	362	9	US-09-779-679-28
14	565	31.9	373	9	US-10-092-135-7
15	562	31.7	365	9	US-10-092-135-5
16	514	29.0	355	9	US-09-077-173A-2
17	488	27.6	334	9	US-10-270-587-2
18	487.5	27.5	330	10	US-09-826-791-2
19	487.5	27.5	346	9	US-09-828-478-2

20	487.5	27.5	346	9	US-09-779-679-2	Sequence 2, Appl1
21	487.5	27.5	346	9	US-09-779-679-26	Sequence 26, Appl1
22	487.5	27.5	346	10	US-09-826-791-6	Sequence 6, Appl1
23	487.5	27.5	346	10	US-09-866-230-7	Sequence 7, Appl1
24	487.5	27.5	346	10	US-09-866-230-9	Sequence 9, Appl1
25	479	27.0	341	9	US-10-270-587-3	Sequence 3, Appl1
26	477	26.9	334	10	US-09-765-034-2	Sequence 2, Appl1
27	426	24.1	317	9	US-09-891-138A-2	Sequence 2, Appl1
28	397	22.4	357	9	US-09-966-755-2	Sequence 2, Appl1
29	397	22.4	357	10	US-09-903-377-2	Sequence 2, Appl1
30	397	22.4	357	10	US-09-952-385-2	Sequence 2, Appl1
31	397	22.4	357	12	US-10-000-759A-2	Sequence 2, Appl1
32	394.5	22.3	339	9	US-09-828-478-4	Sequence 4, Appl1
33	394.5	22.3	339	10	US-09-848-889-12	Sequence 12, Appl1
34	394.5	22.3	339	10	US-09-788-133-2	Sequence 2, Appl1
35	394.5	22.3	357	9	US-09-828-478-6	Sequence 6, Appl1
36	388.5	21.9	425	10	US-09-782-980-80	Sequence 80, Appl1
37	388.5	21.9	425	10	US-09-884-430-4	Sequence 4, Appl1
38	380	21.5	356	9	US-09-779-679-25	Sequence 25, Appl1
39	379.5	21.4	358	9	US-09-885-453-4	Sequence 4, Appl1
40	375.5	21.2	359	9	US-10-094-417-10	Sequence 10, Appl1
41	375.5	21.2	359	9	US-09-782-974C-76	Sequence 76, Appl1
42	375.5	21.2	359	10	US-09-739-151-2	Sequence 2, Appl1
43	372	21.0	302	9	US-10-024-694-30	Sequence 30, Appl1
44	371	20.9	332	9	US-10-001-835-140	Sequence 140, Appl1
45	371	20.9	348	10	US-09-827-937A-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1
US-10-023-775b-2
; Sequence 2, Application US/10023775b
; Publication No. US2003002282A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (EP/GB only)
; APPLICANT: Pfizer Inc. (US, JP, EB except GB)
; APPLICANT: fidock, Mark David
; TITLE OF INVENTION: No. US2003002282A1 Polypeptide
; FILE REFERENCE: PC10959A6PR
; CURRENT APPLICATION NUMBER: US/10/023, 775b
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030854.4
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,590
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/296,660
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: GB 0111031.1
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-023-775b-2
Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDPDYAAAFGKCTDENTLAKMHLPIVYIGIIFLVGFPGNNAVISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAFGKCTDENTLAKMHLPIVYIGIIFLVGFPGNNAVISTYIF 60
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Db 121 ILFLTCFSIFRCYVLIHPMCSFSIHKTRCAVAVCAVWVWISLVAVIMPTFLTISTNRTNR 180
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Db 181 SACLDTSSDELNTIKWNLILFATTCPLPLVITLCTYTIHHTLHGLQDSCLOKAR 240
Qy 241 RLTLILLAFYVCLPFIHLIRIVIRIESRLSISCSIEHQIHEAVIVSRPLAALMTFGNLL 300
Db 241 RLTLILLAFYVCLPFIHLIRIVIRIESRLSISCSIEHQIHEAVIVSRPLAALMTFGNLL 300
Qy 301 LYVVSDNFOQAVCSIVRCCKVSGNLEQAKKISYSNNP 337
Db 301 LYVVSDNFOQAVCSIVRCCKVSGNLEQAKKISYSNNP 337

RESULT 2

US-10-270-144-2

Sequence 2, Application US/10270144

Publication No. US20030045790A1

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: C000750CON

CURRENT APPLICATION NUMBER: US/10/270,144

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/205,196

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 337

TYPE: PRT

ORGANISM: Human

US-10-270-144-2

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 LYVVSDNFOQAVCSIVRCCKVSGNLEQAKKISYSNNP 337

RESULT 3

US-10-188-405-8

Sequence 8, Application US/10188405

Publication No. US20030082585A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long
APPLICANT: Zhao, Jiaqiang
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: NO. US20030082585A1el Receptors
FILE REFERENCE: 018781-008410US
CURRENT APPLICATION NUMBER: US/10/188,405
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/302,800
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 337
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: OTHER INFORMATION: human TGR164

US-10-188-405-8

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 KMRPKSSTIIMLACTDLILYLSPLFIHYVASEGEMWIFGDMCKFIRSFHNLXSS 120
Qy 121 ILFLTCFSIFRCYVLIHPMCSFSIHKTRCAVAVCAVWVWISLVAVIMPTFLTISTNRTNR 180
Db 121 ILFLTCFSIFRCYVLIHPMCSFSIHKTRCAVAVCAVWVWISLVAVIMPTFLTISTNRTNR 180
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Db 301 LYVVSDNFOQAVCSIVRCCKVSGNLEQAKKISYSNNP 337

RESULT 4

US-09-885-453-1

Sequence 1, Application US/09885453

Publication No. US20030088080A1

GENERAL INFORMATION:

APPLICANT: Communal, Didier

TITLE OF INVENTION: RECEPTOR GPCRk10

FILE REFERENCE: 9409/2082

CURRENT APPLICATION NUMBER: US/09/885,453

CURRENT FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: US 09/885,453

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 337

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: amino acid sequence GPCRk10

LOCATION: (1)-(337)

OTHER INFORMATION: GPCRk10 amino acid sequence

US-09-885-453-1

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-943-798-4
; Sequence 4, Application US/09943798
; Patent No. US20020065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: OG1021
; CURRENT APPLICATION NUMBER: US/09/943,798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-943-798-4

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Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNEPDIYLANASDFPDYAAAFGNCNDENIPKMHYLPVYIGIIFLVGFPGNAVISTYIF 60
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DB 181 SACLDITSSDELNTIKWMLILTATTCFLPVIYVLCYTTIIHTLTHGLOTSCLOKAR 240
QY 241 RTIITLLAFYVCFPHILRVIRIESRLISCSIEINOIHEAYISRPALANTFGNLL 300
DB 241 RTIITLLAFYVCFPHILRVIRIESRLISCSIEINOIHEAYISRPALANTFGNLL 300
QY 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYNNP 337
DB 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYNNP 337

DB 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYNNP 337

RESULT 6
US-09-782-974C-86
; Sequence 86, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 g Protein Coupled Receptor
; FILE REFERENCE: 41USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-86

Query Match 90.5%; Score 1602.5; DB 9; Length 336;
Best Local Similarity 92.0%; Pred. No. 5.2e-137;
Matches 312; Conservative 6; Mismatches 14; Indels 7; Gaps 3;

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DB 1 MNEPDIYLANASDFPDYAAAFGNCNDENIPKMHYLPVYIGIIFLVGFPGNAVISTYIF 60
QY 61 KMRPKSSTIIMLNACTDLTLTSLPFLIHYYASGENNIFGDFMCKFRFSHFNLAYS 120
DB 61 KMRPKSSTIIMLNACTDLTLTSLPFLIHYYASGENNIFGDFMCKFRFSHFNLAYS 120
QY 121 IIFLCFSIFRCVYIIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMTFLTSTNRTR 180
DB 121 IIFLCFSIFRCVYIIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMTFLTSTNRTR 180
QY 181 SACLDITSSDELNTIKWMLILTATTCFLPVIYVLCYTTIIHTLTHGLOTSCLOKAR 240
DB 181 SACLDITSSDELNTIKWMLILTATTCFLPVIYVLCYTTIIHTLTHGLOTSCLOKAR 240
QY 241 RTIITLLAFYVCFPHILRVIRIESRLISCSIEINOIHEAYISRPALANTFGNLL 296
DB 241 RTIITLLAFYVCFPHILRVIRIESRLISCSIEINOIHEAYISRPALANTFGNLL 296
QY 297 GNLLLYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYNNP 335
DB 297 GNLLLYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYNNP 335

RESULT 7
US-09-943-798-2
Sequence 2, Application US/09943798
Patent No. US20020065215A1
GENERAL INFORMATION:
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Polypeptide
FILE REFERENCE: OG1021
CURRENT APPLICATION NUMBER: US/09/943,798
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-943-798-2

Query Match 81.5%; Score 1444; DB 10; Length 276;
Best Local Similarity 100.0%; Pred. No. 8,7e-123;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 MRPKSTIIMLNACTDLYLTLPLIHRYASGEMWIRGDEPKFRFSFHNLYSSI 121
DB 1 MRPKSTIIMLNACTDLYLTLPLIHRYASGEMWIRGDEPKFRFSFHNLYSSI 60
QY 122 LFLFCGIFRCVYIIHMSCFSIHKTRCAVAVCAVAVVNIISLVAVIPMTFLITSTNRNRS 181
DB 61 LFLFCGIFRCVYIIHMSCFSIHKTRCAVAVCAVAVVNIISLVAVIPMTFLITSTNRNRS 120
QY 182 ACDDLSDELNTIKWNLILFATFCLPLVITVLCYTTIIHTLHGLQDSCIKOKARR 241
DB 121 ACDDLSDELNTIKWNLILFATFCLPLVITVLCYTTIIHTLHGLQDSCIKOKARR 180
QY 242 LFTLLAFYVCFPHILNRYIRIESRLSISCSIEQNIHAYVSRPALNFGNLL 301
DB 181 LFTLLAFYVCFPHILNRYIRIESRLSISCSIEQNIHAYVSRPALNFGNLL 240
QY 302 YVVVDNFQAVCSTVRCKVSGNLEQAKKISYSNNP 337
DB 241 YVVVDNFQAVCSTVRCKVSGNLEQAKKISYSNNP 276

RESULT 8
US-09-782-974C-60
Sequence 60, Application US/09782974C
Publication No. US20030082534A1
GENERAL INFORMATION:
APPLICANT: Vogel, Gabriel
APPLICANT: Lind, Peter
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
FILE REFERENCE: 41USP8311
CURRENT APPLICATION NUMBER: US/09/782,974C
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/774,449
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-782-974C-60

Query Match 47.0%; Score 831.5; DB 9; Length 192;
Best Local Similarity 86.2%; Pred. No. 1.2e-67;
Matches 168; Conservative 6; Mismatches 14; Indels 7; Gaps 3;

QY 130 FRCVYIIHMSCFSIHKTRCAVAVCAVAVVNIISLVAVIPMTFLITSTNRNRSACLDLTSS 189
DB 1 FRCVYIIHMSCFSIHKTRCAVAVCAVAVVNIISLVAVIPMTFLITSTNRNRSACLDLTSS 60
QY 190 DELNTIKWNLILFATFCLPLVITVLCYTTIIHTLHGLQDSCIKOKARRLITLLIA 249
DB 61 DELNTIKWNLILFATFCLPLVITVLCYTTIIHTLHGLQDSCIKOKARRLITLLIA 120
QY 250 FYVCFDPHILNRYIRIESRLSISCSIEQNIHAYVSRPALNFGNLLYVVV 305
DB 121 FYVCFDPHILNRYIRIESRLSISCSIEQNIHAYVSRPALNFGNLLYVVV 177
QY 306 SDNFQAVCSTVRCK 320
DB 178 SDNFQAVCSTVRCK 192

RESULT 9
US-10-270-144-4
Sequence 4, Application US/10270144
Publication No. US20030049790A1
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CLO00750CON
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 299
TYPE: PRT
ORGANISM: Mus musculus
US-10-270-144-4

Query Match 32.5%; Score 575; DB 9; Length 299;
Best Local Similarity 36.5%; Pred. No. 2.9e-44;
Matches 109; Conservative 67; Mismatches 119; Indels 4; Gaps 2;

QY 24 CTDENIPDKMNYLPVYIGILFVGPQNAVISTYIFKMRPKSSTIIMLNACTDLYL 83
DB 1 CALTKTGFQYYPVAVILVEIIGLGNVAIMFVFMKPMGSIYVMEMLADFLYV 60
QY 84 TSLPDLHYVAGSEMTFGDPKFRFSFHNLYSILFLFCFSIFRCVYIIHMSCFS 143
DB 61 TSLPDLHYVAGSEMTFGDPKFRFSFHNLYSILFLFCFSIFRCVYIIHMSCFS 120
QY 144 IHKTRCAVAVCAVAVVNIISLVAVIPMTFLITSTNRNRS-ACDDLSDELNTIKWNLIL 202
DB 121 LKKNKAIYVSVLVVAVVAVISPILEYSGTGRKKKTVCYTTSNDIYRSFETSMCT 180
QY 203 TATFCLPLVITVLCYTTIIHTLHGLQDSCIKOKARRLITLLIAFYVCFPHILNRY 262

Db 181 TVAMFCIPVLILGCGLVKALIVKALYNDLNSPLRRKSIYLVIVLVFAVSYIPFHVMT 240
 QY 263 IRIESEL---LSISCIENQIHEAVYSRPLAALTFGULLLVVSDNFQAVCSTVR 318
 Db 241 MMLRALDFOFPEMCDENDRYATYQVTRGLASLNSCVPILYFLAGDFRRRLSRATR 299

RESULT 10

US-10-092-135-6
 ; Sequence 6, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; TITLE OF INVENTION: HGPBRMY27
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-10-092-135-6

Query Match 32.0%; Score 567; DB 9; Length 373;
 Best Local Similarity 36.1%; Pred. No. 1,9e-43;
 Matches 108; Conservative 68; Mismatches 119; Indels 4; Gaps 2;

QY 24 CTDENIPKMHYLPVYIGIIFLVGFGNAVVISYIFKMRPMKSTIIMLNACTDLVYL 83
 Db 42 CALTKGFQFYLYPAVYILVFIIFLGNSVAIMFVHMKPMGSIYVMEMLALADFLVY 101
 QY 84 TSLPFLIHYASGEMNIFGDFMCKFRFSFHNLYSILFLCFSLFRICVITIHPSKCS 143
 Db 102 LTLPALIFFYFNKTDIFGDMCKLRFIFHNLYSILFLCFSLAHRSYGVAYPKSLG 161
 QY 144 IHTRCAVAVACAVVWIIISLVAVIPMTFLITSTNRTNRS-ACDLTSSDELNTIKWNLIL 202
 Db 162 RLKKAIAICISVLVWLVVAISPIIFYSTGVRAKKITTCYTTSDEILRSIFITSMCT 221
 QY 203 TATFCELPVIVTLCTYTTIHTLHGLQTDSCIKOKARRLTILLAFYVCELPFHLRY 262
 Db 222 TVAMFCVPLVLIGCYGLVIRALIKDLNLSPLRRKSIYLVIVLVFAVSYIPFHVMT 281
 QY 263 IRIESEL---LSISCIENQIHEAVYSRPLAALTFGULLLVVSDNFQAVCSTVR 318
 Db 282 MMLRALDFOFPEMCDENDRYATYQVTRGLASLNSCVPILYFLAGDFRRRLSRATR 340

RESULT 11

US-10-092-135-3
 ; Sequence 3, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; TITLE OF INVENTION: HGPBRMY27
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: GALLUS GALLUS
 US-10-092-135-3

Query Match 31.9%; Score 565.5; DB 9; Length 362;
 Best Local Similarity 35.0%; Pred. No. 2,6e-43;
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

QY 1 MNEPLDYLANASDEPDYAA---AFGN---CTDENIPKMHYLPVYIGIIFLVGFGNAV 53
 Db 1 MTEALISAALNGTQPELLAGMAAGNASTKCSLTKTGFOFYLYIIVFIFLGNSV 60
 QY 54 VISTYIFKMRPMKSSITIMLNACTDLVLTSLPFLIHYASGEMNIFGDFMCKFRFSF 113
 Db 61 AIMFVFNHMPMGISIVYMNALADFLVLTLPALIFFYFNKTDIFGDMCKLORFIF 120
 QY 114 HFNLYSILFLCFSLFRICVITIHPSKCSIHTRCAVAVACAVVWIIISLVAVIPMTFLI- 172
 Db 121 HVNLYSILFLCFSLFRICVITIHPSKCSIHTRCAVAVACAVVWIIISLVAVIPMTFLI- 180
 QY 173 TSTNRTNRSACDLTSSDELNTIKWNLILFATFCELPVIVTLCTYTTIHTLHGLQTD 232
 Db 181 TGVRRNKTTTCYPTTADVETLRSYFVSMCTYVMEFIPFVILIGCYGLVIRALIKDLN 240
 QY 233 SCLKOKARRLTILLAFYVCELPFHLIRIRIESRL---LSISCIENQIHEAVYSR 289
 Db 241 SPLRRKSIYLVIVLVFAVSYIPFHVMTLMLRALDFOFPEMCDENDRYATYQVTRG 300
 QY 290 IALNFTFGNLLLVVSDNFQAVCSTVR 318
 Db 301 IASLNSCVPILYFLAGDFRRRLSRATR 329

RESULT 12

US-10-092-135-4
 ; Sequence 4, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; TITLE OF INVENTION: HGPBRMY27
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: MELEAGRIS GALLOPAVO
 US-10-092-135-4

Query Match 31.9%; Score 565.5; DB 9; Length 362;
 Best Local Similarity 35.0%; Pred. No. 2,6e-43;
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

QY 1 MNEPLDYLANASDEPDYAA---AFGN---CTDENIPKMHYLPVYIGIIFLVGFGNAV 53
 Db 1 MTEALISAALNGTQPELLAGMAAGNASTKCSLTKTGFOFYLYIIVFIFLGNSV 60
 QY 54 VISTYIFKMRPMKSSITIMLNACTDLVLTSLPFLIHYASGEMNIFGDFMCKFRFSF 113
 Db 61 AIMFVFNHMPMGISIVYMNALADFLVLTLPALIFFYFNKTDIFGDMCKLORFIF 120
 QY 114 HFNLYSILFLCFSLFRICVITIHPSKCSIHTRCAVAVACAVVWIIISLVAVIPMTFLI- 172
 Db 121 HVNLYSILFLCFSLFRICVITIHPSKCSIHTRCAVAVACAVVWIIISLVAVIPMTFLI- 180

RESULT 15
US-10-092-135-5
; Sequence 5, Application US/10092135
; Publication No. US20030054374A1
; GENERAL INFORMATION:
; APPLICATION: Bristol-Myers Squibb Company

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: TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
:
: FILE REFERENCE: D0134.NP
:
: CURRENT APPLICATION NUMBER: US/10/092,135
:
: CURRENT FILING DATE: 2002-03-06
:
: PRIOR APPLICATION NUMBER: US 60/273,808
:
: PRIOR FILING DATE: 2001-03-07
:
: PRIOR APPLICATION NUMBER: US 60/278,983
:
: PRIOR FILING DATE: 2001-03-27
:
: NUMBER OF SEQ ID NOS: 75
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 5
:
: LENGTH: 373
:
: TYPE: PRT
:
: ORGANISM: BOS TAURUS
:
: US-10-092-135-5

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Query Match	31.7%;	Score 562;	DB 9;	Length 373;
Best Local Similarity	36.1%;	Pred. No. 5.5e-43;		
Matches 108; Conservative	67;	Mismatches 120;	Indels 4;	Gaps 2;

QY	24	CTDENIPFLKMHVPIYVIGIIFVPGNAAVSTYIFKRPKSSIIIMLNLACDPLVL	83
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	42	CALRTGSGFYLLPAVYIIVLFIIGLGSVAIMVVFHMKPKSGISVYFNALADPLVY	101
QY	84	TSLDPLIHYVASGENMIFGDMCKPIRESFHENLYSILTECFISYRCVLIHMSCE	143
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	102	LTLPALIIFYENKTEWIMGDMACKQRFETHNLGSLTELCISIAHRRSGVYPLKSI	161
QY	144	IHKPRCAVACAAVWIIISLVAVIPMTFLITSNPNRNS-ACIDTSSDDELNTKWNLLI	202
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	162	RLKKNNAYISVLWMLVAVGISPILFESGTSIRKNKTIYCYDTSDEFLRSFTYS	221
Db	203	TATTFCLPVLIVTLCTYTIHHTLHGLQDTSCLOKARRLTILLLAFVCEPLFI	262
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	222	TVAMCVPVLIVLTCGYGLIVRALIYKDDNSPLRRRSIYIIVLTVFVASYIP	281
QY	263	IRIESRL---LSISISINQIHAEATYSRPLAATMFGULLIYVYSDMFOQAV	318
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	282	MNLRRRLDQPEMKCAFNDRYATAYQVTRKGLASLNSCDPLIYFLAGDIFRRRL	340

Search completed: May 30, 2003, 13:48:22
Job time : 22 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 22:18:54 ; Search time 198 Seconds
(without alignments)
6905.264 Million cell updates/sec

Title: US-10-023-775b-1

Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Published_Applications_NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	100.0	1014	9	US-10-023-775b-1
2	1012.4	99.8	1014	9	US-10-270-144-1
3	1012.4	99.8	1014	9	US-10-188-405-7
4	1012.4	99.8	1014	9	US-09-885-453-2
5	1012.4	99.8	1014	10	US-09-943-798-3
6	1012.4	99.8	9905	9	US-10-270-144-3
7	976.2	96.3	1020	9	US-09-782-974C-85
8	829.4	81.8	831	10	US-09-943-798-1
9	728	71.8	1313	10	US-09-728-422-1
10	537.2	53.0	578	9	US-09-782-974C-59
11	513.4	50.6	526	10	US-09-812-102-40
12	132.8	13.1	1428	9	US-10-812-587-1
13	125	12.3	1543	9	US-09-891-138A-1
14	121.4	12.0	1429	9	US-09-077-173A-1
15	93.6	9.2	993	10	US-09-826-791-1
16	93.6	9.2	1041	9	US-09-828-478-1
17	93.6	9.2	1041	10	US-09-826-791-5
18	93.6	9.2	1041	10	US-09-866-230-6
19	93.6	9.2	1260	9	US-09-779-679-1

20	93.6	9.2	1260	9	US-09-779-679-24	Sequence 24, Appl
21	93.6	9.2	1430	9	US-09-828-478-3	Sequence 3, Appl
22	93.6	9.2	1700	10	US-09-728-952-26	Sequence 26, Appl
23	89.2	8.8	422	9	US-09-779-679-23	Sequence 23, Appl
24	89.2	8.8	1020	10	US-09-788-133-1	Sequence 1, Appl
25	89.2	8.8	1179	9	US-09-930-334-15	Sequence 15, Appl
26	84	8.3	507	9	US-09-782-974C-7	Sequence 7, Appl
27	84	8.3	1670	10	US-09-880-107-2143	Sequence 2143, Ap
28	84	8.3	1737	9	US-09-104-063-3	Sequence 3, Appl
29	82.8	8.2	2051	10	US-09-962-832-218	Sequence 218, App
30	82.8	8.2	2051	10	US-09-944-807-20	Sequence 20, Appl
31	82.6	8.1	1065	9	US-09-922-895-2	Sequence 2, Appl
32	82.6	8.1	1689	10	US-09-931-381A-15	Sequence 15, Appl
33	82.6	8.1	1717	10	US-09-964-824A-100	Sequence 100, App
34	82.6	8.1	1915	12	US-10-106-623-3	Sequence 3, Appl
35	82.6	8.1	3426	9	US-10-001-835-29	Sequence 29, Appl
36	82.4	8.1	1080	10	US-09-739-151-1	Sequence 1, Appl
37	82.4	8.1	1102	9	US-09-870-759-143	Sequence 143, App
38	82.4	8.1	1425	9	US-10-094-417-9	Sequence 9, Appl
39	82.4	8.1	1955	9	US-10-190-469-2	Sequence 2, Appl
40	82.4	8.1	2137	9	US-09-782-974C-75	Sequence 75, Appl
41	81.6	8.0	1112	9	US-09-905-253A-1	Sequence 1, Appl
42	81.6	8.0	2050	9	US-09-940-240-15	Sequence 15, Appl
43	79.8	7.9	1017	9	US-09-885-453-3	Sequence 3, Appl
44	79.6	7.9	1174	9	US-09-930-334-1	Sequence 1, Appl
45	78.8	7.8	1083	10	US-09-852-156-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-023-775b-1
Sequence 1, Application US/10023775B
Publication No. US2003002282A1
GENERAL INFORMATION:
APPLICANT: Pfizer Ltd. (EP/GB only)
APPLICANT: Pfizer Inc. (US, JP, EB except GB)
TITLE OF INVENTION: Mark David
FILE REFERENCE: PCT/0959A/PR
CURRENT APPLICATION NUMBER: US/10/023,775B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: GB 0030854.4
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/260,590
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: US 60/296,660
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: GB 0111031.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-775b-1
Query Match 100.0%; Score 1014; DB 9; Length 1014;
Best local similarity 100.0%; Pred. No. 2.6e-301;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCGATTTCCCGATTATGAGCTGCT 60
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DB 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTCGATTTCCCGATTATGAGCTGCT 60
QY 61 TTGGGAATTCGACTGATGAAACATCCCACTAAATGACACTGCTGCTATTTAT 120
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DB 61 TTGGGAATTCGACTGATGAAACATCCCACTAAATGACACTGCTGCTATTTAT 120
QY 121 GGCATTATCTTCCTCGTGGGATTTCCAGGACGATGATGATTCACATTTTC 180
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Db 121 GGCATATCTCTCTGCGGATTTCCAGGCAATCAGTAGTATATCCATTACATTTTC 180
QY 181 AAATGAGACCTTGGAGAGACGACCATCATTAATGCAAGCTGGCCGACAGATCTG 240
Db 181 AAATGAGACCTTGGAGAGACGACCATCATTAATGCAAGCTGGCCGACAGATCTG 240
QY 241 CTGTATCTGACACCTCCCTCTCTGATTCATAGTATGCGAGTGGGAAAGCTGATC 300
Db 241 CTGTATCTGACACCTCCCTCTCTGATTCATAGTATGCGAGTGGGAAAGCTGATC 300
QY 301 TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 301 TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 ATCCCTTCCCTCACCCTGTTTCAGCATCTCCGCTACTGATGATCATCACCAGTAC 420
Db 361 ATCCCTTCCCTCACCCTGTTTCAGCATCTCCGCTACTGATGATCATCACCAGTAC 420
QY 421 TGCCTTTCATTCACAAACTCGATGTCAGTGTAGCTGTAGCTGTGTGTGTATTC 480
Db 421 TGCCTTTCATTCACAAACTCGATGTCAGTGTAGCTGTAGCTGTGTGTGTATTC 480
QY 481 TCAGTGTAGCTGTATTCGATGACCTTCCTGATTCATGACATGACCAAGGACCAAGA 540
Db 481 TCAGTGTAGCTGTATTCGATGACCTTCCTGATTCATGACATGACCAAGGACCAAGA 540
QY 541 TCAGCTGTCTCGACCTCAGCATGTCGATGATGATGATGATGATGATGATGATG 600
Db 541 TCAGCTGTCTCGACCTCAGCATGTCGATGATGATGATGATGATGATGATGATG 600
QY 601 ATTTGACTGCAATCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 ATTTGACTGCAATCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 ATATTCACACTGTGACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCA 720
Db 661 ATATTCACACTGTGACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCA 720
QY 721 AGGCTAACATTCCTGCTACTCTTGCATTTTACATGATTTTAACTTCAATATCTG 780
Db 721 AGGCTAACATTCCTGCTACTCTTGCATTTTACATGATTTTAACTTCAATATCTG 780
QY 781 AGGCTCATTTGGGATCGAATCTCGCTGCTTCAATGATGATGATGATGATGATG 840
Db 781 AGGCTCATTTGGGATCGAATCTCGCTGCTTCAATGATGATGATGATGATGATG 840
QY 841 CATGAGCTTACATGCTTTCTAGACATTTAGCTGCTGACACCTTTGGTAACTGTTA 900
Db 841 CATGAGCTTACATGCTTTCTAGACATTTAGCTGCTGACACCTTTGGTAACTGTTA 900
QY 901 CTATATGTGTGTGTGACGCAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAA 960
Db 901 CTATATGTGTGTGTGACGCAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAA 960
QY 961 GTAAAGCGGGAACCTTGAGCAAGCAAAATTAATGATTAACCAAAACCTTTGA 1014
Db 961 GTAAAGCGGGAACCTTGAGCAAGCAAAATTAATGATTAACCAAAACCTTTGA 1014

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RESULT 2

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US-10-270-144-1
; Sequence 1, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-1
Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 8e-301;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTGTATTTCCCGATTAATGAGCTGT 60
Db 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTGTATTTCCCGATTAATGAGCTGT 60
QY 61 TTTGGAATTTGCACTGATGAAATATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Db 61 TTTGGAATTTGCACTGATGAAATATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
QY 61 TTTGGAATTTGCACTGATGAAATATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Db 61 TTTGGAATTTGCACTGATGAAATATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
QY 121 GGCATATCTCTCTGCGGATTTCCAGGCAATCAGTAGTATATCCATTACATTTTC 180
Db 121 GGCATATCTCTCTGCGGATTTCCAGGCAATCAGTAGTATATCCATTACATTTTC 180
QY 181 AAATGAGACCTTGGAGAGACGACCATCATTAATGCAAGCTGGCCGACAGATCTG 240
Db 181 AAATGAGACCTTGGAGAGACGACCATCATTAATGCAAGCTGGCCGACAGATCTG 240
QY 241 CTGTATCTGACACCTCCCTCTCTGATTCATAGTATGCGAGTGGGAAAGCTGATC 300
Db 241 CTGTATCTGACACCTCCCTCTCTGATTCATAGTATGCGAGTGGGAAAGCTGATC 300
QY 301 TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 301 TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 ATCCCTTCCCTCACCCTGTTTCAGCATCTCCGCTACTGATGATCATCACCAGTAC 420
Db 361 ATCCCTTCCCTCACCCTGTTTCAGCATCTCCGCTACTGATGATCATCACCAGTAC 420
QY 421 TGCCTTTCATTCACAAACTCGATGTCAGTGTAGCTGTAGCTGTGTGTGTATTC 480
Db 421 TGCCTTTCATTCACAAACTCGATGTCAGTGTAGCTGTAGCTGTGTGTGTATTC 480
QY 481 TCAGTGTAGCTGTATTCGATGACCTTCCTGATTCATGACATGACCAAGGACCAAGA 540
Db 481 TCAGTGTAGCTGTATTCGATGACCTTCCTGATTCATGACATGACCAAGGACCAAGA 540
QY 541 TCAGCTGTCTCGACCTCAGCATGTCGATGATGATGATGATGATGATGATGATG 600
Db 541 TCAGCTGTCTCGACCTCAGCATGTCGATGATGATGATGATGATGATGATGATG 600
QY 601 ATTTGACTGCAATCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 ATTTGACTGCAATCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 ATATTCACACTGTGACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCA 720
Db 661 ATATTCACACTGTGACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGCA 720
QY 721 AGGCTAACATTCCTGCTACTCTTGCATTTTACATGATTTTAACTTCAATATCTG 780
Db 721 AGGCTAACATTCCTGCTACTCTTGCATTTTACATGATTTTAACTTCAATATCTG 780
QY 781 AGGCTCATTTGGGATCGAATCTCGCTGCTTCAATGATGATGATGATGATGATG 840
Db 781 AGGCTCATTTGGGATCGAATCTCGCTGCTTCAATGATGATGATGATGATGATG 840
QY 841 CATGAGCTTACATGCTTTCTAGACATTTAGCTGCTGACACCTTTGGTAACTGTTA 900
Db 841 CATGAGCTTACATGCTTTCTAGACATTTAGCTGCTGACACCTTTGGTAACTGTTA 900
QY 901 CTATATGTGTGTGTGACGCAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAA 960

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Db      121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATATTCACCTTACATTTTC 180
QY      181 AAAATGAGACCTTGGAAAGACAGACCAATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
Db      181 AAAATGAGACCTTGGAAAGACAGACCAATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
QY      241 CTGTATCTGACAGACCTTCCCTTCCTGATTCACCTACTAGTCCAGTGGCGAAAACCTGATC 300
Db      241 CTGTATCTGACAGACCTTCCCTTCCTGATTCACCTACTAGTCCAGTGGCGAAAACCTGATC 300
QY      301 TTGGAGATTTCATGTTAGTTATTCGCTGAGCTTCATTCATTCACCTGTAATAGAGC 360
Db      301 TTGGAGATTTCATGTTAGTTATTCGCTGAGCTTCATTCATTCACCTGTAATAGAGC 360
QY      361 ATCCCTCTCCACCTGTTTCACAGCATCTTCCGCTACTGTGTATCATTCACCAATGAGC 420
Db      361 ATCCCTCTCCACCTGTTTCACAGCATCTTCCGCTACTGTGTATCATTCACCAATGAGC 420
QY      421 TCGTTTTCATTCACAAACTCGATGCAAGTTGACCTGTGCTGTGTGTGTGATCATTT 480
Db      421 TCGTTTTCATTCACAAACTCGATGCAAGTTGACCTGTGCTGTGTGTGTGATCATTT 480
QY      481 TCACGTGATGCTGTCTATCCGATGACCTTCTGATCATCATCAACCAAGACCAACAGA 540
Db      481 TCACGTGATGCTGTCTATCCGATGACCTTCTGATCATCATCAACCAAGACCAACAGA 540
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Db      541 TCAGCCTGTCTGACCTCACACAGTTGAGTGAATCAATATTAAGTGTACAACTTA 600
QY      601 ATTTTACGTGCAACTTCTTCTGCTCCCTTGTGTATGATGACACTTTGCTATACACG 660
Db      601 ATTTTACGTGCAACTTCTTCTGCTCCCTTGTGTATGATGACACTTTGCTATACACG 660
QY      661 ATATTCACACCTGTGACCCATGAGTGAATGCAAGTGCCTTAAAGCAAGAACGCA 720
Db      661 ATATTCACACCTGTGACCCATGAGTGAATGCAAGTGCCTTAAAGCAAGAACGCA 720
QY      721 AGGCTAACCATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCATATCTTG 780
Db      721 AGGCTAACCATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCATATCTTG 780
QY      781 AGGCTATTCGATGCAATCTGCTGCTTTCATCATGTTTTCATGGAATCAGATC 840
Db      781 AGGCTATTCGATGCAATCTGCTGCTTTCATCATGTTTTCATGGAATCAGATC 840
QY      841 CATGAAGCTTACATCTTCTTAGACCATTAAGTGTGCTGTGAAACCTTGTAACTGTTA 900
Db      841 CATGAAGCTTACATCTTCTTAGACCATTAAGTGTGCTGTGAAACCTTGTAACTGTTA 900
QY      901 CTATATGTGTGTGTCAGCGCAACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 960
Db      901 CTATATGTGTGTGTCAGCGCAACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 960
QY      961 GTAAAGGGAGACCTTGAGCAAGCAAGAAATTAAGTACTCAAAACCTTGA 1014
Db      961 GTAAAGGGAGACCTTGAGCAAGCAAGAAATTAAGTACTCAAAACCTTGA 1014

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RESULT 5

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US-09-943-798-3
; Sequence 3, Application US/09/943798
; Patent No. US20020065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: 061021
; CURRENT APPLICATION NUMBER: US/09/943, 798
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1014

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-943-798-3
Query Match      99.88; Score 1012.4; DB 10; Length 1014;
Best Local Similarity 99.98; Pred. No. 8e-301;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATGAATGAGCAGCTAGACATATTAGCAATAGCTTCTGATTTCCCGATATGACAGCT 60
Db      1 ATGAATGAGCAGCTAGACATATTAGCAATAGCTTCTGATTTCCCGATATGACAGCT 60
QY      61 TTGGAAATTTGACCTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
Db      61 TTGGAAATTTGACCTGATGAAACATCCACTCAAGATGCACTACCTCCCTGTTATTTAT 120
QY      121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATATTCACCTTACATTTTC 180
Db      121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGCACTAGTATATTCACCTTACATTTTC 180
QY      181 AAAATGAGACCTTGGAAAGACAGACCAATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
Db      181 AAAATGAGACCTTGGAAAGACAGACCAATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
QY      241 CTGTATCTGACAGACCTTCCCTTCCTGATTCACCTACTAGTCCAGTGGCGAAAACCTGATC 300
Db      241 CTGTATCTGACAGACCTTCCCTTCCTGATTCACCTACTAGTCCAGTGGCGAAAACCTGATC 300
QY      301 TTGGAGATTTCATGTTAGTTATTCGCTGAGCTTCATTCATTCACCTGTAATAGAGC 360
Db      301 TTGGAGATTTCATGTTAGTTATTCGCTGAGCTTCATTCATTCACCTGTAATAGAGC 360
QY      361 ATCCCTCTCCACCTGTTTCACAGCATCTTCCGCTACTGTGTATCATTCACCAATGAGC 420
Db      361 ATCCCTCTCCACCTGTTTCACAGCATCTTCCGCTACTGTGTATCATTCACCAATGAGC 420
QY      421 TCGTTTTCATTCACAAACTCGATGCAAGTTGACCTGTGCTGTGTGTGATCATTT 480
Db      421 TCGTTTTCATTCACAAACTCGATGCAAGTTGACCTGTGCTGTGTGTGATCATTT 480
QY      481 TCACGTGATGCTGTCTATCCGATGACCTTCTGATCATCATCAACCAAGACCAACAGA 540
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QY      541 TCAGCCTGTCTGACCTCACACAGTTGAGTGAATCAATATTAAGTGTACAACTTA 600
Db      541 TCAGCCTGTCTGACCTCACACAGTTGAGTGAATCAATATTAAGTGTACAACTTA 600
QY      601 ATTTTACGTGCAACTTCTTCTGCTCCCTTGTGTATGATGACACTTTGCTATACACG 660
Db      601 ATTTTACGTGCAACTTCTTCTGCTCCCTTGTGTATGATGACACTTTGCTATACACG 660
QY      661 ATATTCACACCTGTGACCCATGAGTGAATGCAAGTGCCTTAAAGCAAGAACGCA 720
Db      661 ATATTCACACCTGTGACCCATGAGTGAATGCAAGTGCCTTAAAGCAAGAACGCA 720
QY      721 AGGCTAACCATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCATATCTTG 780
Db      721 AGGCTAACCATCTGCTACTCTTGTGATTTTACGATGTTTACCTTCATATCTTG 780
QY      781 AGGCTATTCGATGCAATCTGCTGCTTTCATCATGTTTTCATGGAATCAGATC 840
Db      781 AGGCTATTCGATGCAATCTGCTGCTTTCATCATGTTTTCATGGAATCAGATC 840
QY      841 CATGAAGCTTACATCTTCTTAGACCATTAAGTGTGCTGTGAAACCTTGTAACTGTTA 900
Db      841 CATGAAGCTTACATCTTCTTAGACCATTAAGTGTGCTGTGAAACCTTGTAACTGTTA 900
QY      901 CTATATGTGTGTGTCAGCGCAACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 960
Db      901 CTATATGTGTGTGTCAGCGCAACTTTCAGCAGGCTGTCTCTCAACAGTGAATGCAAA 960
QY      961 GTAAAGGGAGACCTTGAGCAAGCAAGAAATTAAGTACTCAAAACCTTGA 1014

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Db 961 GTAAGGGGAACTTGAGCAAGCAAGAAATTAAGTACTCAACACCTTGA 1014
RESULT 6
US-10-270-144-3
; Sequence 3, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9905
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-3
Query Match 99.8%; Score 1012.4; DB 9; Length 9905;
Best Local Similarity 99.9%; Pred. No. 3.3e-300;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 8309 ATGAATGAGCCACTAGACTATTATAGCAAAATGCTTGTGATTTCCCGATTTAGCAGCTGCT 8368
Qy 61 TTGGAAATGACAGTGAAGAAATCCCACTCAAGAGCAGTACTGCTGCTGATTTAT 120
Db 8369 TTGGAAATGACAGTGAAGAAATCCCACTCAAGAGCAGTACTGCTGCTGATTTAT 8428
Qy 121 GGCATTATCTCTGCTGAGGATTTCCAGGCAATGAGTGAATATCCACTAANTTTC 180
Db 8429 GGCATTATCTCTGCTGAGGATTTCCAGGCAATGAGTGAATATCCACTAANTTTC 8488
Qy 181 AAAATGAGACCTTGGAGAGAGCAGACATCATTTATGCTGAGCTGCGACAGATCTG 240
Db 8489 AAAATGAGACCTTGGAGAGAGCAGACATCATTTATGCTGAGCTGCGACAGATCTG 8548
Qy 241 CTGTATCTGACAGCTCCCTCTCTGATCTACTATGCAAGTGGCGAAAACTGGATC 300
Db 8549 CTGTATCTGACAGCTCCCTCTCTGATCTACTATGCAAGTGGCGAAAACTGGATC 8608
Qy 301 TTGGAGATTCATGTGTAAGTTATCCGCTCAGCTTCCATTTCAACTGATATGACAC 360
Db 8609 TTGGAGATTCATGTGTAAGTTATCCGCTCAGCTTCCATTTCAACTGATATGACAC 8668
Qy 361 ATCTCTTCTCAGCTGTTTACAGATCTTCCGCTACTGATGATCATTCACCAATGAGC 420
Db 8669 ATCTCTTCTCAGCTGTTTACAGATCTTCCGCTACTGATGATCATTCACCAATGAGC 8728
Qy 421 TCCCTTTCATTCACAAAATCGAGTGTGAGCTGTGCTGTGTGTGATCATT 480
Db 8729 TCCCTTTCATTCACAAAATCGAGTGTGAGCTGTGCTGTGTGTGATCATT 8788
Qy 481 TCAGTGTGCTGATTCGATTCGATGACCTTGTGATACATCAACCAAGAGCAACAA 540
Db 8789 TCAGTGTGCTGATTCGATTCGATGACCTTGTGATACATCAACCAAGAGCAACAA 8848
Qy 541 TCAGCTGTCTGAGCTCAGAGTTCGATGAGTGAATCAATATTAAGTGTACAACTTA 600
Db 8849 TCAGCTGTCTGAGCTCAGAGTTCGATGAGTGAATCAATATTAAGTGTACAACTTA 8908
Qy 601 ATTTGACTGCAACTACTTGTGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 8909 ATTTGACTGCAACTACTTGTGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 8968

Qy 661 ATTATCCACACTGTGACCCATGAGTCAAACTGACAGCTAGCCTTAAGCAAGAAAGCAGA 720
Db 8969 ATTATCCACACTGTGACCCATGAGTCAAACTGACAGCTAGCCTTAAGCAAGAAAGCAGA 9028
Qy 721 AGGCTAACCATTCCTGCTACTGCTTGTGATTTTACGTAATGTTTATACCTTCATATCTTG 780
Db 9029 AGGCTAACCATTCCTGCTACTGCTTGTGATTTTACGTAATGTTTATACCTTCATATCTTG 9088
Qy 781 AGGCTAACCATTCCTGCTACTGCTTGTGATTTTACGTAATGTTTATACCTTCATATCTTG 840
Db 9089 AGGCTAACCATTCCTGCTACTGCTTGTGATTTTACGTAATGTTTATACCTTCATATCTTG 9148
Qy 841 CATGAAGCTTACATGCTTCTAGACATTAAGCTGCTGTAACACCTTGTGTAACCTGTA 900
Db 9149 CATGAAGCTTACATGCTTCTAGACATTAAGCTGCTGTAACACCTTGTGTAACCTGTA 9208
Qy 901 CTATATGTGTGTGCTGAGCAGCAACTTTCAGCAGGCTGTCTGTCAACAGTGAATGCANA 960
Db 9209 CTATATGTGTGTGCTGAGCAGCAACTTTCAGCAGGCTGTCTGTCAACAGTGAATGCANA 9268
Qy 961 GTAAGGGGAACTTGAGCAAGCAAGAAATTAAGTACTCAACACCTTGA 1014
Db 9269 GTAAGGGGAACTTGAGCAAGCAAGAAATTAAGTACTCAACACCTTGA 9322
RESULT 7
US-09-782-974C-85
; Sequence 85, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: NO. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/186,530
; REMAINING PRIOR APPLICATION data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-85
Query Match 96.3%; Score 976.2; DB 9; Length 1020;
Best Local Similarity 99.4%; Pred. No. 1.1e-289;
Matches 1011; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 ATGAATGAGCCACTAGACTATTATAGCAAAATGCTTGTGATTTCCCGATTTAGCAGCTGCT 60

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Db      64 TTGGAATTTGCACTGATGAAAACATCCACTAGATGACACTACCCCTGTTATTTAT 123
QY      121 GGCATTATCTCTCTCGTGGGATTTCCAGGCAATGACAGTAGTGAATTCACATTATTC 180
Db      124 GGCATTATCTCTCTCGTGGGATTTCCAGGCAATGACAGTAGTGAATTCACATTATTC 183
QY      181 AAAATGAGACCTTGSAAGACACACCATCATATGATGTAACCTGGCGCTCAGAGATCTG 240
Db      184 AAAATGAGACCTTGSAAGACACACCATCATATGATGTAACCTGGCGCTCAGAGATCTG 243
QY      241 CTGTATCTGACACAGCCCTCCCTCTCTGATTCAGTACTATGATCCAGTGGCGAAAACCTGATC 300
Db      244 CTGTATCTGACACAGCCCTCCCTCTCTGATTCAGTACTATGATCCAGTGGCGAAAACCTGATC 303
QY      301 TTGGAATTTGCACTGATGAAAACATCCACTAGATGACACTACCCCTGTTATTTAT 360
Db      304 TTGGAATTTGCACTGATGAAAACATCCACTAGATGACACTACCCCTGTTATTTAT 363
QY      361 ATCCCTTCTCTCAGCTGTTTACAGATCTTCCGCTACTGTTGATTCATTCACCAATGAGC 420
Db      364 ATCCCTTCTCTCAGCTGTTTACAGATCTTCCGCTACTGTTGATTCATTCACCAATGAGC 423
QY      421 TGCCTTTCCATTCACAAAACCTGATGTCAGTTGAGCCTGTGCTGGTGGTGGATCAT 480
Db      424 TGCCTTTCCATTCACAAAACCTGATGTCAGTTGAGCCTGTGCTGGTGGTGGATCAT 483
QY      481 TCAGCTGATGCTGATCCGATTCGATGACCTTCTGATCATCAACAACAGAGCAACAGA 540
Db      484 TCAGCTGATGCTGATCCGATTCGATGACCTTCTGATCATCAACAACAGAGCAACAGA 543
QY      541 TCAGCTGATGCTGATCCGATTCGATGACCTTCTGATCATCAACAACAGAGCAACAGA 600
Db      544 TCAGCTGATGCTGATCCGATTCGATGACCTTCTGATCATCAACAACAGAGCAACAGA 603
QY      601 ATTTTACTGCAACTACTTCTGCTCTCCCTTGGTGTATGATGACACTTTCCTTATTCACAG 660
Db      604 ATTTTACTGCAACTACTTCTGCTCTCCCTTGGTGTATGATGACACTTTCCTTATTCACAG 663
QY      661 ATTTATCCACTCTGACCCATGAGAGTGAACACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
Db      664 ATTTATCCACTCTGACCCATGAGAGTGAACACTGACAGCTGCTTAAAGCAGAAAGCAGA 723
QY      721 AGGCTAACCATCTGCTACTCCTTGCATTTTACGTATGTTTATACCTTCCATTCATCTTG 780
Db      724 AGGCTAACCATCTGCTACTCCTTGCATTTTACGTATGTTTATACCTTCCATTCATCTTG 783
QY      781 AGGCTAACCTC-GGATCGAATCTC-GCCTGCTTTCATCATGTTGTTCCATTTGAGAAATCAGA 838
Db      784 AGGCTAACCTCAGAGTGAATCTCAGCCTGCTTTCATCATGTTGTTCCATTTGAGAAATCAGA 843
QY      839 TCCATTAAGCTTACATCTGTTTCTAGACATTA-GCTGCTCTGAACACCTTGGTAACTCG 897
Db      844 TCCATTAAGCTTACATCTGTTTCTAGACATTAAGCTGCTCTGAACACCTTGGTAACTCG 903
QY      898 TTACTATATGCTGCTGACGACCACTTTCAGCAGGCTGTGCTGCAACAGAGATGTC 957
Db      904 TTACTATATGCTGCTGACGACCACTTTCAGCAGGCTGTGCTGCAACAGAGATGTC 963
QY      958 AAAGTAAAGCGGAGACCTTGAGCAAGCAAGAAATAGTTACTCAACAACCTTGA 1014
Db      964 AAAGTAAAGCGGAGACCTTGAGCAAGCAAGAAATAGTTACTCAACAACCTTGA 1020

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RESULT 8
 US-09-943-798-1
 ; Sequence 1, Application US/09943798
 ; Patent No. US20020065215A1
 ; GENERAL INFORMATION:

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; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: OG1021
; CURRENT APPLICATION NUMBER: US/09/943,798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ. ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO 1
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-943-798-1

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Query Match 81.8%; Score 829.4; DB 10; Length 831;

Best Local Similarity 99.9%; Pred. No. 1,4e-244;

Matches 830; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      184 ATGAGACCTTGGAAAGACACACATCATATGCTGAACCTGGCTGACAGATCTGCTG 243
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QY      244 TATCTGACAGCCCTCCCTCTGATTCAGTACTATGATGAGCCAGTGGCGAAAACCTGATCTTT 303
Db      61 TATCTGACAGCCCTCCCTCTGATTCAGTACTATGATGAGCCAGTGGCGAAAACCTGATCTTT 120
QY      304 GGAGATTTCACTGATGTAAGTTTATCCGCTTCAGCTTCATTCACCTGATATGACAGATC 363
Db      121 GGAGATTTCACTGATGTAAGTTTATCCGCTTCAGCTTCATTCACCTGATATGACAGATC 180
QY      364 CTCTTCTCTACCTGTTTACAGATCTTCCGCTACTGTTGATTCATTCACCAATGAGCTGC 423
Db      181 CTCTTCTCTACCTGTTTACAGATCTTCCGCTACTGTTGATTCATTCACCAATGAGCTGC 240
QY      424 TTTTCATTCACAAAACCTGATGAGGATGAGCTGAGCGCTGCTGGTGGATCATTTCA 483
Db      241 TTTTCATTCACAAAACCTGATGAGGATGAGCTGAGCGCTGCTGGTGGATCATTTCA 300
QY      484 CTGTAGCTGCTGATCCGATGACCTTCTGATCATCAACAACAGAGCAACAGATCA 543
Db      301 CTGTAGCTGCTGATCCGATGACCTTCTGATCATCAACAACAGAGCAACAGATCA 360
QY      544 GCTCTGCTGACCTCAGCAGTGTGGATGAACTCAATATCTTAAAGTGTGCAACCTTAAT 603
Db      361 GCTCTGCTGACCTCAGCAGTGTGGATGAACTCAATATCTTAAAGTGTGCAACCTTAAT 420
QY      604 TTGACGCAACTACTTCTGCTCTCCCTTGGTGTATGATGACACTTGTGATACAGATTT 663
Db      421 TTGACGCAACTACTTCTGCTCTCCCTTGGTGTATGATGACACTTGTGATACAGATTT 480
QY      664 ATCCACACTCTGACCATGAGATGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGAAG 723
Db      481 ATCCACACTCTGACCATGAGATGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGAAG 540
QY      724 CTACCATCTCTGCTACTCCTTGCATTTTACGTATGTTTATACCTTCCATTCATCTTGAG 783
Db      541 CTACCATCTCTGCTACTCCTTGCATTTTACGTATGTTTATACCTTCCATTCATCTTGAG 600
QY      784 GTCATTCGAGTGAATCTGCGCTGTTTCAATAGTGTTCATGAGATGAGATCATCAT 843
Db      601 GTCATTCGAGTGAATCTGCGCTGTTTCAATAGTGTTCATGAGATGAGATCATCAT 660
QY      844 GAAGCTTACATCTGTTCTAGACCATTAAGTCTCTGAACACCTTGGTAACTGTTACTA 903
Db      661 GAAGCTTACATCTGTTCTAGACCATTAAGTCTCTGAACACCTTGGTAACTGTTACTA 720
QY      904 TATGTGCTGCTGACGACCACTTTCAGCAGGCTGTGCTCAACAACATGAGATGCAAGTA 963
Db      721 TATGTGCTGCTGACGACCACTTTCAGCAGGCTGTGCTCAACAACATGAGATGCAAGTA 780
QY      964 AGCGGGAACCTTGAGCAAGCAAGAAATAGTTACTCAACAACCTTGA 1014
Db      781 AGCGGGAACCTTGAGCAAGCAAGAAATAGTTACTCAACAACCTTGA 831

```

RESULT 9

US-09-728-422-1
; Sequence 1, Application US/09728422
; Patent No. US20020128187A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020128187A1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 787CIP2F
; CURRENT APPLICATION NUMBER: US/09/728,422
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 1
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (547)..(1239)
US-09-728-422-1

Query Match 71.8%; Score 728; DB 10; Length 1313;
Best Local Similarity 99.7%; Pred. No. 2,9e-213;
Matches 740; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 ATGATGAGGCGACTAGACATTTTACGAATGCTTGTGATTTCCCGCATTTATGACGCTCT 60
DB 547 ATGAAATGAGGCGACTAGACATTTTACGAATGCTTGTGATTTCCCGCATTTATGACGCTCT 606
QY 61 TTGGAAATGCGCTAGTAAATCCCAATGCAATGACATGACATGCTCCCTGTTATTTAT 120
DB 607 TTGGAAATGCGCTAGTAAATCCCAATGCAATGACATGACATGCTCCCTGTTATTTAT 666
QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGACATGATGATATCCACTTACATTTTC 180
DB 667 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGACATGATGATATCCACTTACATTTTC 726
QY 181 AAATAGACCTTGGAAAGACGACACCATCATTTATGCTGAACCTGGCTGACACAGATCTG 240
DB 727 AAATAGACCTTGGAAAGACGACACCATCATTTATGCTGAACCTGGCTGACACAGATCTG 786
QY 241 CCGTATCTGACGCGCTCCCTCCGATGATGATGATGATGATGATGATGATGATGATGATG 300
DB 787 CCGTATCTGACGCGCTCCCTCCGATGATGATGATGATGATGATGATGATGATGATGATG 846
QY 301 TTGGAGATTTTCAATGTAAGTTTATCCGCTTCCAGCTTCCATTTCAACCTGTATAGACG 360
DB 847 TTGGAGATTTTCAATGTAAGTTTATCCGCTTCCAGCTTCCATTTCAACCTGTATAGACG 966
QY 361 ATCCCTTCTCCACCTGTTTACAGATCTTCCGCTTCCAGCTTCCATTTCAACCTGTATAG 420
DB 907 ATCCCTTCTCCACCTGTTTACAGATCTTCCGCTTCCAGCTTCCATTTCAACCTGTATAG 966
QY 421 TGGTTTTCATTTACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 967 TGGTTTTCATTTACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATG 1026
QY 481 TCACTGGTACGTCTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

RESULT 10

US-09-782-974C-59/C
; Sequence 59, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/144,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-59

Query Match 53.0%; Score 537.2; DB 9; Length 578;
Best Local Similarity 99.0%; Pred. No. 8.7e-155;
Matches 572; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 387 CTTCGCTACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 446
DB 578 CTTCGCTACTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 519
QY 447 TGCAGTTGAGCCTGTGCTGT 506
DB 518 TGCAGTTGAGCCTGTGCTGT 459

QY 507 CTCTTGATCATTCAACCAACAGACCAAGATACACCTGTCTGACCTCACCAGTTC 566
 DB 458 CTCTTGATCATTCAACCAACAGACCAAGATACACCTGTCTGACCTCACCAGTTC 399
 QY 567 GGATGAACTCACTACTATTAAGTGTACACCTAATTTTGGACTGCACTACTTCTGCT 626
 DB 398 GGATGAACTCACTACTATTAAGTGTACACCTAATTTTGGACTGCACTACTTCTGCT 339
 QY 627 CCCCTGGTGTAGTGTACACTTTGTATACCAAGTATATCCACACTGTGACCAATGAGCT 686
 DB 338 CCCCTGGTGTAGTGTACACTTTGTATACCAAGTATATCCACACTGTGACCAATGAGCT 279
 QY 687 GCAAACTGACAGCTGCTTAAAGCAGAAAGCAGAGGCTTAACTTCTGCTACTCTTGC 746
 DB 278 GCAAACTGACAGCTGCTTAAAGCAGAAAGCAGAGGCTTAACTTCTGCTACTCTTGC 219
 QY 747 ATTTTACATGATTTTATACCTTCCATATCTTGAGGCTATTC-6GATGCAATCTC-6C 804
 DB 218 ATTTTACATGATTTTATACCTTCCATATCTTGAGGCTATTC-6GATGCAATCTC-6C 159
 QY 805 CTGCTTCAATCAGTGTGTCCATGTAGATGAGATCCATGAGCTTACATGCTTCTAGA 864
 DB 158 CTGCTTCAATCAGTGTGTCCATGTAGATGAGATCCATGAGCTTACATGCTTCTAGA 99
 QY 865 CCAATTA-GCTGCTGTGAACACCTTTGGTAACTTACTATATGTGTGTGACGACAA 923
 DB 98 CCAATTAAGTCTGTGAACACCTTTGGTAACTTACTATATGTGTGTGACGACAA 39
 QY 924 CTTTACAGAGCTGTCTGCTCAACAGATGAGATGCAAG 961
 DB 38 CTTTACAGAGCTGTCTGCTCAACAGATGAGATGCAAG 1

RESULT 11

US-09-812-102-40/C
 : Sequence 40, Application US/09812102
 : Patent No. US20020055179A1
 : GENERAL INFORMATION:
 : APPLICANT: Robison, Keith E
 : TITLE OF INVENTION: No. US20020055179A1el G-Protein Coupled Receptor Homologs
 : FILE REFERENCE: 5800-41 035800/183478
 : CURRENT APPLICATION NUMBER: US/09/812,102
 : CURRENT FILING DATE: 2001-03-19
 : PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/364,769
 : PRIOR FILING DATE: 1999-07-30
 : NUMBER OF SEQ ID NOS: 90
 : SOFTWARE: Patentln Ver. 2.0
 : SEQ ID NO 40
 : LENGTH: 526
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : OTHER INFORMATION: GPCR-RHODOPSIN
 US-09-812-102-40

Query Match 50.6%; Score 513.4; DB 10; Length 526;
 Best Local Similarity 99.8%; Pred. No. 1.7e-147;
 Matches 514; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 259 CCCCTCTGATCTACTATGCGAGTGGGAAAAGTGGATCTTTGGAGATTCATGTCT 318
 DB 526 CCCCTCTGATCTACTATGCGAGTGGGAAAAGTGGATCTTTGGAGATTCATGTCT 467
 QY 319 AAGTTATCGGCTCAGCTCCATTCATGACCTGTATGAGCAATCCCTTCCACCTGCT 378
 DB 466 AAGTTATCGGCTCAGCTCCATTCATGACCTGTATGAGCAATCCCTTCCACCTGCT 407
 QY 379 TTGAGCATCTCCGCTACTGTGTGATCATTCACCAATGAGCTGCTTTCCATTCACAAA 438
 DB 406 TTGAGCATCTCCGCTACTGTGTGATCATTCACCAATGAGCTGCTTTCCATTCACAAA 347
 QY 439 ACTGATGTGCAAGTTGTAAGCTGTGTGTGTGTGATCATTCATGTAAGTGTGATTT 498

DB 346 ACTGATGTGCAAGTTGTAAGCTGTGTGTGTGATCATTCATGTAAGTGTGATTT 287
 QY 499 CCGATGACCTCTTGATGATCAATCAACCAAGGACCAACATGACCTGTCTGACCTC 558
 DB 286 CCGATGACCTCTTGATGATCAATCAACCAAGGACCAACATGACCTGTCTGACCTC 227
 QY 559 ACCAGTTGGATGTAAGTCAATATTAAGTGTATCAACCAATTTTGGACTGCAACTACT 618
 DB 226 ACCAGTTGGATGTAAGTCAATATTAAGTGTATCAACCAATTTTGGACTGCAACTACT 167
 QY 619 TTCTGCTCCCTTGGTGTATAGTGAACACTTTGTATATACAGATTTATCCACTGTGAC 678
 DB 166 TTCTGCTCCCTTGGTGTATAGTGAACACTTTGTATATACAGATTTATCCACTGTGAC 107
 QY 679 CATGAGTGCAAAGCTGACAGCTGCTTAAAGCAGAAAGCAGAGGCTTAACTTCTGCTA 738
 DB 106 CATGAGTGCAAAGCTGACAGCTGCTTAAAGCAGAAAGCAGAGGCTTAACTTCTGCTA 47
 QY 739 CTCTTGATTTTACGATATGTTTAACTTCCA 773
 DB 46 CTCTTGATTTTACGATATGTTTAACTTCCA 12

RESULT 12

US-10-270-587-1
 : Sequence 1, Application US/10270587
 : Publication No. US20030054487A1
 : GENERAL INFORMATION:
 : APPLICANT: Li, Yi
 : TITLE OF INVENTION: Human G-Protein Coupled Receptor
 : FILE REFERENCE: PF217C2
 : CURRENT APPLICATION NUMBER: US/10/270,587
 : CURRENT FILING DATE: 2002-10-16
 : PRIOR APPLICATION NUMBER: US 09/908,593
 : PRIOR FILING DATE: 2001-07-20
 : PRIOR APPLICATION NUMBER: US 08/781,456
 : PRIOR FILING DATE: 1997-01-10
 : PRIOR APPLICATION NUMBER: US 60/009,902
 : PRIOR FILING DATE: 1996-01-11
 : NUMBER OF SEQ ID NOS: 9
 : SOFTWARE: Patentln version 3.1
 : SEQ ID NO 1
 : LENGTH: 1428
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-10-270-587-1

Query Match 13.1%; Score 132.8; DB 9; Length 1428;
 Best Local Similarity 49.4%; Pred. No. 3.9e-30;
 Matches 437; Conservative 0; Mismatches 432; Indels 15; Gaps 3;

QY 55 GCTGCTTTTGGAAATGTCACATGATGAAGAAATCCCACTCAAGATGACCTACCTCCGT 114
 DB 116 GCAACTTGCAAAAATGCTGCGACGACAGAGCTGCTCGGAAAAGTACTACTTTCATT 175
 QY 115 ATTAATGGAATTAATCTCTGCTGTGGATTTCCAGCAATGCAAGTATGATCCACTTAC 174
 DB 176 TTTTATGGAATGATGCTGTGTGTGGAGTCTCTGGAATATGCAATGTGTGTTACGGCTAC 235
 QY 175 ATTTTCAAAATGAGACCTTGGAGAGACGACACCATCATATATGCTGAACCTGGCTGACA 234
 DB 235 GATGTGCTGATCTGACACGCTCCCTTCTGATTTACATATGCAATGCGAGGAAC 294
 QY 236 ATCTTCTCTCTGAAGAACTGGAAGCAGCAATATATTTATCTTAACTCTCTGTCTCT 295
 DB 296 GACTTAACCTTTCTGTGACACCTCCCATCTGTGTAAGAGATTAGCAATG--AAAC 352
 QY 295 TGAATCTTTGAGATTGATGATGTAAGTTATCCGCTTACGCTTCAATTCACCTGAT 354
 DB 353 TGAATATATGAGACGCTGCTGTGATATGAGAACCAACGATATGTGCTTACATGCAACCTAT 412
 QY 355 AGCAGATCTCTTCTACACCTTTTACAGATCTTCGCTACTGTGTGATCATTCACCA 414

[illegible]

Db	60	CTTGTGAGAAATGGTGTGGCAACAGAGGCTATCTTGAATAGTACTACCTCTGACATTTT	111
Qy	119	ATGGCATTAATCTTCTCTGTGGATTTCCAGGCATCAGTAGTATATCCATTACTTTT	111
Db	120	ATGCATATCAGATTCATTTTGTGGACCTCTTGGGAATATCTACTGTGGTTCGGCTACTT	111
Qy	179	TCAAAATGAGACCTTGGAGAGAGACACATCTATTATGCGAATCGGCGCTGACAGATC	111
Db	180	TCGTGATGAAACATGGAACAGAGGAATGCTATCTTTTAACCTTTTCATCTTGACT	111
Qy	239	TGCTGTATGTGACCAACCTCCCTCTCTGATTCATCTACTATGCGAGTGGCAAACTGA	111
Db	240	TTCGCTTTCGTGGACACCTTCCATCTGTATTAAGATTATGCAAT--GATTAAGGGA	111
Qy	299	TCTTTGGACATTTCAATGTGTAACTTTATCCGCTTCAGCTTCCATTCAACCTGTATGA	111
Db	297	CCATATGGAATATGTCCTGTATATGAACACCGAATATGTCTTACACCAACCTCTACCA	111
Qy	359	GCATCTCTTCCGACACCTGTTTATGACATCTCCGTACTGTGATCATTCACCCATGA	111
Db	357	GCATCTCTTCCCTCACTTTCATTAGCATGAGACCGAATATGCTCATGAAAGTACCTTTCC	111
Qy	419	GCTGCTTTTCCATTCACAAATCGATGTGATGTGACATTTAGCGTGTGCTGTGATCA	111
Db	417	GAGAACACTTTGTACAAAAGAAAGAAATTTGCCATTTTAATCTCGGTGCTGTGGGCT	111
Qy	479	TTTCACTGTAGCTGTCATTTCCGATGACCTTTCTTAATCACAATCAACCAAGACCAACA	111
Db	477	TAGTGACCTTAGAAGTTCTAACCCATCTCACTTTCATCAATTTCTGCCAAAAGAGAG	111
Qy	539	GATCAGCCGTCTCGACCTCACCAAGTTCG-----ATGAACATACATATAAGTGT	111
Db	537	GGATGATGACATCTGACATATGCAAGTCTTGAAACCTTGACACAAATCTCATTTACAGCC	111
Qy	593	ACAACCTAATTTTGAATGCTGCAACTACTTTTGCCTCCCTCTGATAGTATGACACTTTGCT	111
Db	597	TCTGCTGACTTTGTGGGCTTCCATATCTCTCTCTGTGATGTGCTTCTTACTACA	111
Qy	653	ATACACGATTAATCCACACTGTGACCCATGAGATGCAAACTGACAGCTGCTTAAGACA	111
Db	657	AGATGTAGTCTTCTTAAGAGAGAGAGACAGACAGCAAGCAATGCCCTCCACTGGACA	111
Qy	713	AAGCAGAGAGGCTAACCATTTCTGCTACTCTTTCATTTTACGATATGTTTTTACCCTTC	111
Db	711	AACCCCAAGCGCTGGTGGTCTGGCGGTGTGTATCTTCTATATCTTTCACACCTATC	111
Qy	773	ATATCTTGAAGGTCATTCGGATCGAATCTGCCTG 807	111
Db	777	ATATCATGCGCAATTTGAGAGATGCGCTCACGCTG 811	111
RESULT 14			
Sequence 1, Application US/09077173A-1			
Publication No. US20030082674A1			
GENERAL INFORMATION:			
APPLICANT:			
TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING			
TITLE OF INVENTION: SAID RECEPTOR			
NUMBER OF SEQUENCES: 4			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/077,173A			
FILING DATE:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: WO PCT/BE 96/00123			
FILING DATE:			
INFORMATION FOR SEQ ID NO: 1:			

SEQUENCE CHARACTERISTICS:
 LENGTH: 1429 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 181..1275
 US-09-077-173A-1

Query Match 12.0%; Score 121.4; DB 9; Length 1429;
 Best Local Similarity 51.0%; Pred. No. 1.2e-26;
 Matches 287; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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OY 92 TCAGATGACTACCTCCCTGTTATTTATGCACTTATCTCCCTGGGATTTCCAGCA 151
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Db 278 TCAGATGACTACCTCCCTGTTATTTATGCACTTATCTCCCTGGGATTTCCAGCA 151
OY 152 ATGAGTAGATATCCACTTACATTTTCAAAATGAGACCTTGAAGAGCAGCACAATCA 211
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 338 AGGCCCAACCCCTATGCGCTTTCATCTCCGCTCCGACCCCTGGAGAGCAACGGCAGCT 397
OY 212 TTATGCTGAACCTGGCTGCGACAGATCTGCTGTATCTGACAGCCTCCCTCTGATTC 271
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 398 ACATGCTTCACCTGGCATGTGTCAGACACCTGTATGTGCTGCTGCCGCCACCTCATCT 457
OY 272 ACTACTATGCCAGTGGGAAACTGATCTTTGGAGATTTGATGTTATTCGCT 331
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 458 ACTATATGAGAGCCACACACACTGCGCTTTGGCACTGAGATCTGCAAGTCTCGCT 517
OY 332 TCACCTTCCATTTCAACCTGTATAGCAGACATCTCTTCTTCCACCTGTTTCAGATCTCC 391
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 518 TTTCTTTCTTATGGAACCTCTACTGAGTGTCTTTTCTTCCACCTGATCAGCTGACCC 577
OY 392 GCTACTGTGATCATTCACCCATGAGCTGCTTTTCCATTCACAAAACCTGAGTGCAG 451
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 578 GCTACTGTGATCATTCACCCATGAGCTGCTTTTCCATTCACAAAACCTGAGTGCAG 451
OY 452 TTGAGCCTGTGCTGTGTGATGATTCATTTCACTGATGATGATTCGATTCGATTCCT 511
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Db 638 GCTCTCTGCTGCTGAGTTTGTGTGTCGATGAGCGGCTGCTGCTGCTGCTGCTGCT 697
OY 512 TGATCAGATCAACCAAGAGCAGACAGATGAGCTGTCTGACCTCAGCAGTTGGATG 571
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 698 TTGTCACACACAGCAGACAAAGGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGAG 757
OY 572 AACTGATATATTAAGTGTGACAACTAATTTGACTGCAACTACTTTCTGCTCCCT 631
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 758 AGTTGACCACTATGCTCACTTCAGCTGCGGCTGATGAGGCTGCTCTTGGCTGCCCT 817
OY 632 TGGTATATGACACTTTGCTAT 654
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 818 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

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RESULT 15
 US-09-826-791-1

; Sequence 1, Application US/09826791
 ; Patent No. US20010039037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc
 ; TITLE OF INVENTION: No. US20010039037A1 Polypeptide
 ; FILE REFERENCE: PCI0914ADAM
 ; CURRENT APPLICATION NUMBER: US/09/826,791
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 0008504.3
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: 60/198,367
 ; PRIOR FILING DATE: 2000-04-19
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent Ver. 2.0
 ; SEQ. ID NO 1

; LENGTH: 993
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-826-791-1

Query Match 9.2%; Score 93.6; DB 10; Length 993;
 Best Local Similarity 52.3%; Pred. No. 3.6e-18;
 Matches 207; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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OY 92 TCAGATGACTACCTCCCTGTTATTTATGCACTTATCTCCCTGGGATTTCCAGCA 151
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Db 59 TCAGAGAGAGATTTTTCATTTGATATGATATATTTTCTGGGAGTCTTGGGAA 118
OY 152 ATGAGTAGATATCCACTTACATTTTCAAAATGAGACCTTGAAGAGCAGCACAATCA 211
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 119 ATGGGTTGCTCATATATGTTTCTGACAGCTTATAGAGTCAATCTGTGAGCTTT 178
OY 212 TTATGCTGAACCTGGCTGCGACAGATCTGCTGTATCTGACAGCCTCCCTCTGATTC 271
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 179 TCATGCTAAATCTGGCATTTTCAATCTCTGTTCAATAGCAGCCTTCCCTCAGGGCTG 238
OY 272 ACTACTATGCCAGTGGGAAACTGATCTTTGAGATTTTCAATGATTAATTCGCT 331
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 239 ACTATATCTTGAAGCTCCATTTGATTTGAGAGCTGCGCTGCGAGGATTAATGCTT 298
OY 332 TCAGCTTCAATTTCAACCTGTATAGCAGATCTCTTCTCACCTGTTTCCAGATCTTCC 391
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 299 ATTCTTGTATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 358
OY 392 GCTACTGTGATCATTCACCCATGAGTGTCTTTTCCATTCACAAAACCTGATGTCAG 451
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 359 GTTTCCTGGAATGTTTCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418
OY 452 TTGAGCCTGTGCTGTGTGATGATTCATTTCACTGG 487
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Db 419 GATCTCTGTGGATATATGATGATCTTATCATAG 454

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Search completed: May 29, 2003, 23:45:05
 Job time : 200 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:43:23 ; Search time 27 Seconds
(without alignments)
367.242 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPDIYLANSDFPDYAA.....RCVSGNLEQAKKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents, AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564.5	31.9	362	3	US-08-513-974B-374 Sequence 374, App
2	562	31.7	373	2	US-08-559-524A-4 Sequence 4, App11
3	562	31.7	373	3	US-08-749-707-4 Sequence 4, App11
4	477	26.9	373	3	US-08-513-974B-373 Sequence 373, App
5	467	26.4	334	2	US-08-559-524A-2 Sequence 2, App11
6	467	26.4	334	3	US-08-749-707-2 Sequence 2, App11
7	438	24.7	375	1	US-08-442-134A-2 Sequence 2, App11
8	438	24.7	375	1	US-08-444-581B-2 Sequence 2, App11
9	438	24.7	375	1	US-08-446-088A-2 Sequence 2, App11
10	438	24.7	375	2	US-08-559-524A-3 Sequence 3, App11
11	438	24.7	375	3	US-08-749-707-3 Sequence 3, App11
12	421	23.8	328	3	US-08-513-974B-39 Sequence 39, App1
13	421	23.8	328	3	US-08-513-974B-371 Sequence 371, App
14	406.5	23.0	327	3	US-08-513-974B-372 Sequence 372, App
15	404	22.8	357	5	PCT-US95-07180-3 Sequence 3, App11
16	400	22.6	328	3	US-08-513-974B-56 Sequence 56, App1
17	400	22.6	328	3	US-08-513-974B-360 Sequence 360, App
18	397	22.4	357	4	US-09-266-464-2 Sequence 2, App11
19	394.5	22.3	339	2	US-08-153-848-44 Sequence 44, App1
20	394.5	22.3	339	2	US-08-812-871-3 Sequence 3, App11
21	394.5	22.3	339	3	US-09-299-843B-44 Sequence 44, App1
22	394.5	22.3	339	4	US-09-088-337B-44 Sequence 44, App1
23	394.5	22.3	339	5	PCT-US93-11153-44 Sequence 44, App1
24	394.5	22.3	339	5	PCT-US95-07180-2 Sequence 2, App11
25	391.5	22.1	395	1	US-08-097-938-5 Sequence 5, App11
26	391.5	22.1	395	1	US-08-476-000-5 Sequence 5, App11
27	391.5	22.1	395	1	US-08-472-840-5 Sequence 5, App11

28	391.5	22.1	395	2	US-08-476-976-5 Sequence 5, App11
29	391.5	22.1	395	3	US-08-474-410-5 Sequence 5, App11
30	388.5	21.9	328	3	US-08-459-046-2 Sequence 2, App11
31	388.5	21.9	395	4	US-08-486-673B-2 Sequence 2, App11
32	388.5	21.9	395	4	US-08-486-673B-5 Sequence 5, App11
33	388.5	21.9	399	1	US-08-476-000-61 Sequence 61, App1
34	388.5	21.9	399	1	US-08-472-840-61 Sequence 61, App1
35	388.5	21.9	399	2	US-08-476-976-61 Sequence 61, App1
36	388.5	21.9	399	3	US-08-474-410-61 Sequence 61, App1
37	388.5	21.9	399	4	US-08-486-673B-61 Sequence 61, App1
38	388.5	21.9	425	1	US-07-657-769B-69 Sequence 69, App1
39	388.5	21.9	425	1	US-08-097-938-7 Sequence 7, App11
40	388.5	21.9	425	1	US-08-313-553-13 Sequence 13, App1
41	388.5	21.9	425	1	US-07-789-184-220 Sequence 220, App
42	388.5	21.9	425	1	US-08-476-000-7 Sequence 7, App11
43	388.5	21.9	425	1	US-08-475-263-220 Sequence 220, App
44	388.5	21.9	425	1	US-08-472-840-7 Sequence 7, App11
45	388.5	21.9	425	1	US-08-485-886-220 Sequence 220, App

ALIGNMENTS

RESULT 1
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357

FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-374

Query Match 31.9%; Score 564.5; DB 3; Length 362;
Best Local Similarity 35.0%; Pred. No. 9.1e-37;

Matches 115; Conservative 66; Mismatches 135; Indels 11; Gaps 4;

QY 1 MNEPLDILANASDPDYAA--AFGN---CTDENIPDKMHYLPVIGIIFLVGFPGNAV 53
DB 1 MNEPLDILANASDPDYAA--AFGN---CTDENIPDKMHYLPVIGIIFLVGFPGNAV 53
QY 54 VISTYFKMRPMKSTTLMNLAETDILVLTSLPFLIHVYASGENWTFEGMCKTFRSF 113
DB 61 AINMFVPMRPMKSTTLMNLAETDILVLTSLPFLIHVYASGENWTFEGMCKTFRSF 120
QY 114 HENLYSILFLGCEIFRYCVIITHPMSCFISIKTRCAVAVACAVMIISLVAVIPMTLIT 173
DB 121 HENLYSILFLGCEIFRYCVIITHPMSCFISIKTRCAVAVACAVMIISLVAVIPMTLIT 180
QY 174 STNRTRS-ACLDLTSDELNTIKMYNLITATTFCPLVIVLCYTTIHTLTHGLQTD 232
DB 181 IGRNRKTTCYDTFADYLRSYFVSMCTVEMFCIPYIIGCYLILKALIKRLDN 240
QY 233 SCUKARRLTILLALAFYVCFPLPHILAVIRIESRL--LSISCSIEQIHEAYIVSRP 289
DB 241 SPLRRKSTYLVITLVFAVSYLPFHVMTLNLRARLDFQTPQMCANRKYVATYVTRG 300
QY 290 LALNTEGNNLLTVVSDNQOAVCSIVR 318
DB 301 LALNTEGNNLLTVVSDNQOAVCSIVR 329

RESULT 2
US-08-559-524A-4
Sequence 4, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4

Query Match 31.7%; Score 562; DB 2; Length 373;
Best Local Similarity 36.1%; Pred. No. 1.5e-36;
Matches 108; Conservative 67; Mismatches 120; Indels 4; Gaps 2;

QY 24 CTDENIPDKMHYLPVIGIIFLVGFPGNAVISTYIFKMRPMKSTTLMNLAETDILYL 83
DB 42 CALTKGTFQFYPAVYILVFIIGLGNVAIMMFVPMRPMKSTTLMNLAETDILYL 101
QY 84 TSLPFLIHVYASGENWTFEGMCKTFRSFPHNLYSILFLGCEIFRYCVIITHPMSCFS 143
DB 102 LTLPALFYFNKTDWTFEGMCKTFRSFPHNLYSILFLGCEIFRYCVIITHPMSCFS 161
QY 144 IHTRCVAVACAVMIISLVAVIPMTLITSTNRTRS-ACLDLTSDELNTIKMYNLIL 202
DB 162 RLKKNVAVISLVAVIPMTLITSTNRTRS-ACLDLTSDELNTIKMYNLIL 221
QY 203 TATTFCPLVIVLCYTTIHTLTHGLQTDSCUKARRLTILLALAFYVCFPLPHILAV 262
DB 222 TVAMFCVPLVILIGCYLILKALIKRLDNLSPLRRKSTYLVITLVFAVSYLPFHVMT 281
QY 263 IRIESRL--LSISCSIEQIHEAYIVSRPLALNTEGNNLLTVVSDNQOAVCSIVR 318
DB 282 MNLARLDFQTPQMCANRKYVATYVTRGLASLNSCVPLILFLAGDTRRLSRATR 340

RESULT 3
US-08-749-707-4
Sequence 4, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

RESULT 5

US-08-559-524A-2

; Sequence 2, Application US/08559524A

; Patent No. 5871963

; GENERAL INFORMATION:

; APPLICANT: Conley, Pamela B.

; APPLICANT: Jantzen, Hans-Michael

; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

; STREET: 1800 M Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5869

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/559, 524A

; FILING DATE: 15-NOV-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Adler, Reid G.

; REGISTRATION NUMBER: 30,988

; REFERENCE/DOCKET NUMBER: 044481-5010-00-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-467-7000

; TELEFAX: 202-467-7176

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 334 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-559-524A-2

Query Match 26.4%; Score 467; DB 2; Length 334;

Best Local Similarity 35.3%; Pred. No. 3.2e-29;

Matches 108; Conservative 61; Mismatches 125; Indels 12; Gaps 6;

```
QY 23 NCIDEN-----IPKMHYLPVYIGIIFLVGPPGNAVVISYIFKMRPKSSTIMLNLAC 77
DB 8 NATCKNMLAAEALAEKYYLSIFYGIEFVGVGLNTIVVGYIFSLKMNSSNIYLFMLSV 67
QY 78 TDLIYLSLPELILHYVASEGNWIFGDMCKFIRESFHNLYSSILFTCSIFRYCYIHH 137
DB 68 SDLAFLCTLPMLIRSYANG-NWIIYGDVLCISNRIVLHANLYTSLFTFISIDRYLLIKY 126
QY 138 PMSCFSIHKTRCAVAVCAVVMIIISLAVIPMTFLITSTNRTNSACIDLTSDELNTIKW 197
DB 127 PFEHLLQKKEFALLISLAIWLVLTLELPLILPLINVIITDNGTTCDFPSSGDPNNLI 186
QY 198 YNLIATFTFCPLPVYITLCYTTI-IHTLHGLOTDSCLK-QKARRLTILLALLAFYVCF 255
DB 187 YSMCLTLLGLPLPLFVWCFFYYKIALFLKQRNRQVATAPLEKPLNVLINAVVIFSVLFT 246
QY 256 PFHILVIRIESRLS---ISCSIEHQIHEAVTVSRPLALNFGNLLLVVVSNDNQQA 312
DB 247 PYHVMNRVIRASRLSGWKQYQCT-QVYINSFYIVTRALGLNSVINPVFFELGDDHRDM 305
QY 313 VCSTVR 318
DB 306 LMMQLR 311
```

RESULT 6
US-08-749-707-2

; Sequence 2, Application US/08749707

; Patent No. 6063582

; GENERAL INFORMATION:

; APPLICANT: Conley, Pamela B.

; APPLICANT: Jantzen, Hans-Michael

; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP

; STREET: 1800 M Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20036-5869

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/749,707

; FILING DATE: 15-NOV-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Adler, Reid G.

; REGISTRATION NUMBER: 30,988

; REFERENCE/DOCKET NUMBER: 044481-5010-01-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-467-7000

; TELEFAX: 202-467-7176

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 334 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-749-707-2

Query Match 26.4%; Score 467; DB 3; Length 334;

Best Local Similarity 35.3%; Pred. No. 3.2e-29;

Matches 108; Conservative 61; Mismatches 125; Indels 12; Gaps 6;

```
QY 23 NCIDEN-----IPKMHYLPVYIGIIFLVGPPGNAVVISYIFKMRPKSSTIMLNLAC 77
DB 8 NATCKNMLAAEALAEKYYLSIFYGIEFVGVGLNTIVVGYIFSLKMNSSNIYLFMLSV 67
QY 78 TDLIYLSLPELILHYVASEGNWIFGDMCKFIRESFHNLYSSILFTCSIFRYCYIHH 137
DB 68 SDLAFLCTLPMLIRSYANG-NWIIYGDVLCISNRIVLHANLYTSLFTFISIDRYLLIKY 126
QY 138 PMSCFSIHKTRCAVAVCAVVMIIISLAVIPMTFLITSTNRTNSACIDLTSDELNTIKW 197
DB 127 PFEHLLQKKEFALLISLAIWLVLTLELPLILPLINVIITDNGTTCDFPSSGDPNNLI 186
QY 198 YNLIATFTFCPLPVYITLCYTTI-IHTLHGLOTDSCLK-QKARRLTILLALLAFYVCF 255
DB 187 YSMCLTLLGLPLPLFVWCFFYYKIALFLKQRNRQVATAPLEKPLNVLINAVVIFSVLFT 246
QY 256 PFHILVIRIESRLS---ISCSIEHQIHEAVTVSRPLALNFGNLLLVVVSNDNQQA 312
DB 247 PYHVMNRVIRASRLSGWKQYQCT-QVYINSFYIVTRALGLNSVINPVFFELGDDHRDM 305
QY 313 VCSTVR 318
DB 306 LMMQLR 311
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RESULT 7
US-08-442-134A-2
; Sequence 2, Application US/08442134A
; Patent No. 5596088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.

```

APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
-ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 3607836th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/442,134
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sidley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-581B-2

Query Match          24.7%; Score 438; DB 1; Length 375;
Best Local Similarity 33.0%; Pred.No. 6.3e-27;
Matches 93; Conservative 59; Mismatches 118; Indels 12; Gaps 4.

QY      28 NIPKMYLPIYTGILFLVGFPPGNAVISTITFKRPFKSSITIMLNACDLDLYLTSLP 87
       |  |||:::|  |||  ::::|  |||  ::::|  |||  ::::|  |||  ::::|
Db      28 NEDEKYLLPVSYGVVCVLGLCLNVAAGYLIFLCRLKTWNASTTYFHILAVSDALAAASLP 87
       |  |||:::|  |||  ::::|  |||  ::::|  |||  ::::|  |||  ::::|

QY      88 FLIHYYAGEWIMGDFCKFIREFSHFNLSIILFCFSIFRCVLIHPMSCPSIKHT 147
       :  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|
Db      88 LLVITYTAGDMWPSTYLVCKLRPLFYTNLCSIIILFCISYHRGLGVRPLRSIRMGRA 147
       :  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|

QY      148 RCAYVACAVMWIISLVAVIPTFTLTSNTNRNSACDLDTSSDELINTIKWMLILTATTF 207
       |  |||:::|  |||  ::::|  |||  ::::|  |||  ::::|  |||  ::::|
Db      148 RYARVARVAGAWVWLVIACQAPVLYFVTBAR-GPLTCHDTPSAPELFSRRVAYSVMGLLF 206
       |  |||:::|  |||  ::::|  |||  ::::|  |||  ::::|  |||  ::::|

QY      208 CLPLVITYTLCTTTIHL-----THGLQTDSCLOKAKRRTILLALLAFYCFELPHIL 260
       :  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|
Db      207 AVPRAVTVLVCVLMARRLKPAYGTSGGLPR--AKRRSVETIAVVLAVALFALCFDPFHYT 263
       :  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|  ::|||:::|

QY      261 RVIRIESRLGISCIENQHAEATVSRLAALNTFGULXY 302
       |  |||:::|  |||  ::::|  |||  ::::|  |||  ::::|  |||  ::::|
Db      264 RTLYYSFRSLDISCHTLNAIMATKYTR-LASANSCLDDPVLT 304
       |  |||:::|  |||  ::::|  |||  ::::|  |||  ::::|  |||  ::::|

RESULT 9
US-08-446-088A-2
Sequence 2, Application US/08446088A
Patent No. 5691156
GENERAL INFORMATION:
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Query Match	24.7%;	Score 438;	DB 2;	Length 375;
Best Local Similarity	33.0%;	Pred. No. 6.3e-27;		
Matches	93;	Conservative	59;	Mismatches 118;
			Indels	12;
			Gaps	4

Qy	28	NIDLKMHVYDVIYGIIFELVGFQPNNAVISTYIEFKRPMKSSIIIMLNLACGDDLLYTSP	87
Db	28	NEDKRYLVLPVSGVGVCGVGLCLINAVGLIIFCLIKLTNAASTTYEHLAVSDALYKASP	87
Qy	88	FLIHYYASGENMIFGDGCKETRFSEFHNLYSSILFCTGSIERYCVIIHPMCSPIHKT	147
Db	88	LLYYIYARGDHMFPSFVLCKLWFLFETYLMLYCIIIFLACISIVHRCGLVRLPRLSLMGRA	144
Qy	148	RCNVVACAVWIIISLAVIPMTFLITSTNRTNRASCIDLTSGDELNTIKWNLILFATTF	207
Db	148	KYKRRVAGAVWVYLWLCQAPVLYETTSAR -GRLCHDTSAPLEFSRVAYSVMGLIF	206
Qy	208	CLEPLVITVLCQYTIHITL-----THGLOTDSCLKORARLLTILLALFYVCEPFEHL	266
Db	207	AVPEAVILVCYVLMARLLKPAYGSGGLPR---AKRSVRIAVLAVLAFCELPHEVT	265
Qy	261	KVIRIESRLIISGSIENQIHKAYISRLALNFPGNLLY	302
Db	264	RTLYISFRSLDSCITLAINNAVKTR -LASANSCDLPVLX	304

RESULT 11
 US-08-749-707-3
 Sequence 3, Application US/08749707
 Patent No. 6063582
 GENERAL INFORMATION:
 APPLICANT: Conley, Pamela B.
 APPLICANT: Jantzen, Hans-Michael
 TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington

Query Match	24.7%	Score 438	DB 3	Length 375
Best Local Similarity	33.0%	Pred. No. 6.3e-27		
Matches 93	Conservative 59	Mismatches 118	Indels 12	Gaps 4

RESULT 12
US-08-513-974B-39
; Sequence 39, Application US/08513974B

APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ohtsaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhiko
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 City: Boston
 STATE: MA
 COUNTRY: USA

```

      ZIP: 02109
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/513,974B
      FILING DATE: 14-SEP-1995
      CLASSIFICATION: 536
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: PCT/JP95/01599
      FILING DATE: 10-AUG-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 7-093989
      FILING DATE: 19-AUG-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 7-057186
      FILING DATE: 16-MAR-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 7-007177
      FILING DATE: 20-JAN-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-326611
      FILING DATE: 28-DEC-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-270017
      FILING DATE: 02-NOV-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-236357
      FILING DATE: 30-SEP-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-236356
      FILING DATE: 30-SEP-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-189274
      FILING DATE: 11-AUG-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-189273
      FILING DATE: 11-AUG-1945
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: JP 6-189272
      FILING DATE: 11-AUG-1994
      ATTORNEY/AGENT INFORMATION:
      NAME: Resnick, David S.
      REGISTRATION NUMBER: 34,235
      REFERENCE/DOCKET NUMBER: 45753
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617-523-3400
      TELEFAX: 617-523-6440
      INFORMATION FOR SEQ ID NO: 39:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 328 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      US-08-513-974B-39

Query Match      23.8%; Score 421; DB 3; Length 328;
Best Local Similarity 32.9%; Pred. No. 1,2e-25;
Matches 96; Conservative 45; Mismatches 125; Indels 26; Gaps 5;

OY      36 LPVYIGILFLVGFPGNAVISTYTFKMRPKMSSTIMUNLACTDLILYISLPELHYAS 95
Db      29 LTPVYIVLVVGLFPLNCVIAQICASRTLTNSAVYTLNLALADLMWACSLPLIYNYAR 88
OY      96 GENNIFPDGDMCKFRFSFHFNLYSILFLTCFSIFRCVLIHHPMSCFSIHK---TRCAVY 152
Db      89 GDHHPFDGDLACRFRLFYALNHSILFLTICISFORYLIGICHLA--SMHKRGGRRAWY 146
OY      153 ACAVWVITSLAVAVIPMTFLITSTNRNRSACLDITSSDELTNIKWNILATATTCPLV 212
Db      153 ACAVWVITSLAVAVIPMTFLITSTNRNRSACLDITSSDELTNIKWNILATATTCPLV 212

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Db 147 VCGVWLVATVTAOCLPFAVFAATGIQRNRVTCYDLSPIILSTRILPYGMALTVIGFLPFI 206
QY 213 IIVLCYTTIHTLTHGLQTDSC-----LKOKARRLTLLLAIFYVCFLLPHIL 260
Db 207 ALLACVORMARL-----CRDGPAGVAGQERRSKARMAVVAAYVAISFLPHIT 258
QY 261 RVIRIESRL-SISCSISNOIHEAVYSRPLAALNTFGLNLLVYVSDNFQO 311
Db 259 KTAIVAVRSTPGVSCPVLETFMAAYKGTREFAVSNSVLDPLIFYFTQOKFR 310

RESULT 13
US-08-513-974B-371
; Sequence 371, Application US/08513974B
; Patent No. 6114139

GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380

CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272

; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-6440
; TELEFAX: 617-523-3400
; INFORMATION FOR SEQ ID NO: 371:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-513-974B-371

Query Match 23.8%; Score 421; DB 3; Length 328;
Best Local Similarity 32.9%; Pred. No. 1.2e-25;
Matches 96; Conservative 45; Mismatches 125; Indels 26; Gaps 5;

QY 36 LPVYIGTIFLVGPPGNAVISTYIFKMRPMKSSITILNLAAGTDLTYLSPLFIHYAS 95
Db 29 LTFVYSVVLVVGGLPINCIVIAQICASRRITRSVYTLNLADLMAAGSLPLIYAR 88
QY 96 GEMWIFGDMCKTIFRSFHNLYSSILFLCFSTFRYCVTIHPMSCFSIHK---TRCAV 152
Db 89 GDHMFEDGLACRFVRFLEFVNLHGSILFLCISFRYLGICHPLA--SWHKGGRRAVY 146
QY 153 ACAVWIIISLVAVIPKFLTSTNRTNRACDLTSSDELNTKWNLLITATFCPLV 212
Db 147 VCGVWLVATVTAOCLPFAVFAATGIQRNRVTCYDLSPIILSTRILPYGMALTVIGFLPFI 206
QY 213 IIVLCYTTIHTLTHGLQTDSC-----LKOKARRLTLLLAIFYVCFLLPHIL 260
Db 207 ALLACVORMARL-----CRDGPAGVAGQERRSKARMAVVAAYVAISFLPHIT 258
QY 261 RVIRIESRL-SISCSISNOIHEAVYSRPLAALNTFGLNLLVYVSDNFQO 311
Db 259 KTAIVAVRSTPGVSCPVLETFMAAYKGTREFAVSNSVLDPLIFYFTQOKFR 310

RESULT 14
US-08-513-974B-372
; Sequence 372, Application US/08513974B
; Patent No. 6114139

GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380

CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599

FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-227017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 372:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 327 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-513-974B-372

Query Match 23.0%; Score 406.5; DB 3; Length 327;
 Best Local Similarity 33.8%; Pred. No. 1.5e-24;
 Matches 96; Conservative 46; Mismatches 131; Indels 11; Gaps 6;

QY 36 LPVYIGITFLVGFPGNAVISTYIFKMRPKSSITIMNLACTDLILYTSPLFIHYA 95
 DB 29 LTPVSVYLVVGLPLNICVIAQICASRRTLRSAVYTLMLADLMTACSLPLLYNAR 88
 QY 96 GENMIFGDMCKFRFSEFNLYSILFLCFISIRYCVIHPMCSFSTHK--TRCAVY 152
 DB 89 CDHMFPGDLACRFVFLRYANLHGSILFLTCISPRYIGICHPLA--SWHKKGRRAMV 146
 QY 153 ACAVWI-ISLVAVIPMTFLITSTNRNSACLDLTSDELNTIKMYNLITATFCPL 211
 DB 147 VGVVWLVAVTAQCLTAFAFAATGIOR-NRTVCYDLSPLISRYLPYGALVIGPLPF 205
 QY 212 VIVITLCYTTIIHTLHGQTDSCLOK---KARLITLILLALVYCFPLPHILIRIESR 268
 DB 206 IALLACYCMARRLCRDGPAGVPAQERSKARMAVAAVAISFLPHITKTYAVLR 265
 QY 269 IL-SISCSIEQNIHEAYIVSRPLALNTFGNLLVWVSDNQO 311
 DB 266 STPGVSCVLETFAAATKGTREFASVNSVLDPLITFYTOOKRR 309

RESULT 15

PCT-US95-07180-3
 Sequence 3, Application PC/TUS9507180
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: GOCAYNE, JEANINE D
 APPLICANT: RUBEN, STEVEN M
 TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBER69
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NJ
 COUNTRY: US
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07180
 FILING DATE: 06-JUNE-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 30,073
 REFERENCE/DOCKET NUMBER: 325800-366
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1744
 TELEFAX: 201-994-1700
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-07180-3

Query Match 22.8%; Score 404; DB 5; Length 357;
 Best Local Similarity 30.3%; Pred. No. 2.6e-24;
 Matches 89; Conservative 72; Mismatches 125; Indels 8; Gaps 5;

QY 35 YLPVYIGITFLVGFPGNAVISTYIFKMRPKSSITIMNLACTDLILYTSPLFIHYA 94
 DB 42 FMPSVYTVIFIVSLPLNVLAVFVLRMKVKKPAAVYMLHMLADVLFSVLPKISYXF 101
 QY 95 GENMIFGDMCKFRFSEFNLYSILFLCFISIRYCVIHPMCSFSTHK--TRCAVY 154
 DB 102 SGTDMFGSGMCRFATAAYIWMYASIMLATVYISIDRLAVYPIIOSLSWRLLGANFTC 161
 QY 155 AVWIIISLVAVIPMTFLITSTNR--NRSACLDLTSDELNTI-KMYNLITATFCPL 210
 DB 162 VIVWVAVMGVPL-LKRGQTRVPGNLNTTCHDLSLMLMGFSYVSARSALFEFLVP 220
 QY 211 VIVITLCYTTIIHTLHGQTDSCLOKARRITLILLALFYCFPLPHILIRIESRL 270
 DB 221 LIVSVYCYYSIIRCLSSSAVANRSKSRALFLSAVFCIFVCFGTNLLLVHY--LEL 278
 QY 271 SISCSIEQNIHEAYIVSRPLALNTFGNLLVWVSDNQOAVGSRCKVSGN 324
 DB 279 SDSPTGE-AAVFAVILCVYTSVSCCIDPLIITYYASSSECRLYSLTCKESSD 331

Search completed: May 30, 2003, 13:47:54
 Job time : 28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 21:37:48 ; Search time 2792 Seconds

(without alignments)
10569.572 Million cell updates/sec

Title: US-10-023-775B-1

Perfect score: 1014
Sequence: 1 atgatgagccactagacta.....gttactcaaacaccccttga 1014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	100.0	1014	6	AX305130 Sequence
2	1014	100.0	1014	6	AX464561 Sequence
3	1012.4	99.8	1014	6	AX148186 Sequence
4	1012.4	99.8	1014	6	AX379468 Sequence
5	1012.4	99.8	1014	6	AX384211 Sequence
6	1012.4	99.8	1014	6	AB083598 Homo sapi
7	1012.4	99.8	1014	9	AF411109 Homo sapi
8	1012.4	99.8	1081	6	AX458238 Sequence
9	1012.4	99.8	1092	9	AF370886 Homo sapi
10	1012.4	99.8	1414	9	AB065877 Homo sapi
11	1012.4	99.8	9905	6	AX379470 Sequence
12	1012.4	99.8	67645	9	AL356486 Human DNA
13	1012.4	99.8	156555	9	AC026756 Homo sapi
14	1010.8	99.7	1729	6	AX191332 Sequence
15	976.2	96.3	1020	6	AX147840 Sequence
16	735.6	72.5	202838	2	AC108794 Mus muscu
17	537.2	53.0	578	6	AX147814 Sequence
18	332	32.7	2245	6	AX384210 Sequence
19	189	18.6	657	6	AX244775 Sequence
20	161.2	15.9	1977	5	AF031897 Metleagris
21	158.6	15.6	1293	10	MM022829 Mus muscu
22	158.6	15.6	3204	10	MM022830 Mus muscu
23	153.8	15.2	12630	10	MM0245636 Mus muscu
24	153.8	15.2	288763	2	AC124692 Mus muscu
25	148.6	14.7	1312	9	S81950 P2 purinoc
26	148.6	14.7	1426	9	HS042029 Human P2Y1
27	148.6	14.7	2424	9	HS042030 Human P2Y1
28	148.6	14.7	16178	2	AC021662 Homo sapi
29	148.6	14.7	176170	2	AC021662 Homo sapi
30	148.6	14.7	176251	9	AC013251 Homo sapi
31	147.6	14.6	73949	2	AC105795 Rattus no
32	147	14.5	1308	4	BT034041 Bos taurus
33	147	14.5	1666	4	BT02YRECIP Rattus no
34	144.2	14.2	2231	5	AF242850 Rattus no
35	143	14.1	2951	5	AF432354 Xenopus l
36	134.8	13.3	1163	5	GDP2Y3 AL590151 zebrafish
37	134.2	13.2	136930	5	AF069555 Metleagris
38	133.2	13.1	1074	5	AF069555 Metleagris
39	132.6	13.1	3055	9	HSATPRMR 249205 H. sapiens m
40	130.8	12.9	2361	5	G28604 human STS S
41	130.8	12.9	91107	2	AC116265 Rattus no
42	129.8	12.8	192524	2	AC120742 Rattus no
43	129.8	12.8	209273	2	AC121579 Mus muscu
44	129.6	12.8	1325	9	AF247785 Homo sapi
45	129.6	12.8	1325	9	AF247785 Homo sapi

ALIGNMENTS

RESULT 1	AX305130	1014 bp	DNA	linear	PAT 11-DEC-2001
LOCUS	AX305130	Sequence 10 from Patent WO0187937.			
DEFINITION	AX305130				
ACCESSION	AX305130				
VERSION	AX305130.1	GI:17644765			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens.				
REFERENCE					
AUTHORS	Patterson,C., Lu,D.A., Thornton,M., Lu,Y., Tribouley,C.M., Grau,R., Khan,F.A., Gandhi,A.R., Walla,N.K., Nguyen,D.B., Yue,H., Hafalla,A., Elliott,V.S., Lal,P., Reddy,R., Kallick,D.A., Tang,T.Y.				

Pred. No. is the number of results predicted by chance to have a

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OY 541 TCAGCTGATGCTGATTCGATGACCTTCTGATACATCAACCAAGACAGACAGAGA 600
Db 541 TCAGCTGATGCTGATTCGATGACCTTCTGATACATCAACCAAGACAGACAGAGA 600
OY 601 ATTTGACACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 660
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OY 661 ATTATCCACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 720
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Db 721 AGGCTAACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 780
OY 781 AGGCTAACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 840
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OY 841 CATGAAGCTTACATGCTTCTAGACATTAAGTCTGTAACACTTTCCTTACACAG 900
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Db 901 CTATATGCTGCTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 960
OY 961 GTAAAGGGAACCTTGAAGCAAGAAATAGTACTCAACAACCTTGA 1014
Db 961 GTAAAGGGAACCTTGAAGCAAGAAATAGTACTCAACAACCTTGA 1014

RESULT 3
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LOCUS AX148186
DEFINITION Sequence 27 from Patent WO0136471.
ACCESSION AX148186
VERSION AX148186.1 GI:14347086
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Chen, R., Pang, H.T. and Lowitz, K.P.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
receptors
JOURNAL Patent: WO 0136471-A 27 25-MAY-2001;
ARENA Pharmaceuticals, Inc. (US)
FEATURES
source 1. 1014
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 258 a 263 c 189 g 304 t
ORIGIN

Query Match 99.8%; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.9%; Pred. No. 2,3e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels ~ 0; Gaps 0;

OY 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTGCT 60
Db 1 ATGAATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGACGCTGCT 60
OY 61 TTGGAAATGCACTATGAAATCAATCCCAATGACATGACATGACATGCTTCTATTTAT 120
Db 61 TTGGAAATGCACTATGAAATCAATCCCAATGACATGACATGACATGCTTCTATTTAT 120
OY 121 GGCATTATCTTCCCTGCGGATTTCCAGCAATGACATGATTCACACTTACATTTTC 180

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OY 181 AAATAGACCTTGGAAAGACAGACACATATATGATGAACTGGCTGACAGACAGCTG 240
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Db 241 CTGATCTGACAGACCTCCCTTCCGATTCAGTACATGACAGTGGAGCAAACTGATC 300
OY 301 TTGGAGATTTCAATGATGATTAAGTTATCCGCTTACGCTTCAATTTCAACCTGTA 360
Db 301 TTGGAGATTTCAATGATGATTAAGTTATCCGCTTACGCTTCAATTTCAACCTGTA 360
OY 361 ATCTCTCTCTACAGCTTTCACATCTTCCGCTGATGCTGATGATGATGATGATGAT 420
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OY 421 TGGCTTTTCATCAAAAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
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Db 481 TCAGCTGATGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
OY 541 TCAGCTGATGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 TCAGCTGATGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
OY 601 ATTTGACACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 660
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Db 661 ATTATCCACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 720
OY 721 AGGCTAACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 780
Db 721 AGGCTAACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 780
OY 781 AGGCTAACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 840
Db 781 AGGCTAACACTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 840
OY 841 CATGAAGCTTACATGCTTCTAGACATTAAGTCTGTAACACTTTCCTTACACAG 900
Db 841 CATGAAGCTTACATGCTTCTAGACATTAAGTCTGTAACACTTTCCTTACACAG 900
OY 901 CTATATGCTGCTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 960
Db 901 CTATATGCTGCTGATTCGATTCGCTCCCTTGGTATAGTACACTTTCCTTACACAG 960
OY 961 GTAAAGGGAACCTTGAAGCAAGAAATAGTACTCAACAACCTTGA 1014
Db 961 GTAAAGGGAACCTTGAAGCAAGAAATAGTACTCAACAACCTTGA 1014

RESULT 4
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LOCUS AX379468
DEFINITION Sequence 1 from Patent WO0187980.
ACCESSION AX379468
VERSION AX379468.1 GI:19575226
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Wei, M.H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and

Beasley, E.M.
Isolated human g-protein coupled receptors, nucleic acid molecules
encoding human gpcr proteins, and uses thereof
Patent: WO 0187980-A 1 22-NOV-2001;
Applera Corporation Robert A. Millman Assistant Secretary (US)

FEATURES
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Best Local Similarity 99.98; Pred. No. 2.3e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 5 from Patent WO0214511.
ACCESSION AX384211
VERSION AX384211.1 GI:19577652
KEYWORDS
SOURCE human.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Ramakrishnan, S.
TITLE Regulation of human p2y1-like g protein-coupled receptor
JOURNAL Patent: WO 0214511-A 5 21-FEB-2002;
Bayer Aktiengesellschaft (DE)
location/Qualifiers

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BASE COUNT 258 a 263 c 189 g 304 t
ORIGIN

Query Match 99.88; Score 1012.4; DB 6; Length 1014;
Best Local Similarity 99.98; Pred. No. 2.3e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 LOCUS AB083598 Homo sapiens GPCR gene for putative G-protein coupled receptor.
 DEFINITION complete cds, clone:hGPCR16.
 ACCESSION AB083598
 VERSION AB083598.1 GI:20152259
 KEYWORDS
 SOURCE Homo sapiens DNA, clone:hGPCR16.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Takeda,S., Kadowaki,S., Haga,T., Takaesu,H. and Mitaku,S.
 TITLE Identification of G protein-coupled receptor genes from the human genome sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1014)
 AUTHORS Takeda,S., Kadowaki,S., Haga,T., Takaesu,H. and Mitaku,S.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-2002) Shigeaki Takeda, Gunma University, Department of Biological and Chemical Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan (E-mail:stakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434, Fax:+81-277-30-1434)
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 BASE COUNT 258 a 263 c 189 g 304 t
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 Best Local Similarity 99.9%; Pred. No. 2,3e-257;
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LOCUS Homo sapiens G protein-coupled receptor (GPR80) gene, complete cds.
DEFINITION AF411109
ACCESSION AF411109.1 GI:16566322
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
MEDLINE 21458557
PUBMED 11574155
REFERENCE 2 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of
Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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BASE COUNT 258 a 263 c 189 g 304 t
ORIGIN
Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best local Similarity 99.9%; Pred. No. 2.3e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGAGCGCACTATAGCAAAATGCTTCGATTTCCCGCATTTAGCAGCTGCT 60
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LOCUS AX458238
DEFINITION Sequence 1 from Patent W00246414.
ACCESSION AX458238
VERSION AX458238.1 GI:21724972
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and Ryssek, R.P.
 TITLE A novel human g-protein coupled receptor, hgrprmy23, expressed highly in kidney
 JOURNAL Patent: WO 0246414-A 1 13-JUN-2002;
 Bristol-Myers Squibb Company (US)
 FEATURES
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 BASE COUNT 280 a 277 c 198 g 326 t
 ORIGIN
 Query Match 99.8%; Score 1012.4; DB 6; Length 1081;
 Best Local Similarity 99.9%; Pred. No. 2.3e-257;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 LOCUS Homo sapiens g protein-coupled receptor GPR99 (GPR99) mRNA,
 DEFINITION complete cds.
 ACCESSION AF370886
 VERSION AF370886.1 GI:21728283
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1092)
 Wittenberger, T., Hellebrand, S., Munc, A., Kretschamp, H.J.,
 Schaller, H.C. and Hampe, W.
 GPR99, a new g-protein-coupled receptor belonging to a new subgroup
 of nucleotide receptors
 BMC Genomics 3 (1), 17 (2002)
 2 (bases 1 to 1092)
 Hampe, W.
 Direct Submission
 Submitted (17-APR-2001) Developmental Neurobiology, Zentrum fuer
 Molekulare Neurobiologie, Martinstr. Hamburg 20246, Germany
 JOURNAL
 TITLE
 AUTHORS
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 JOURNAL
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Dp	19	ATGATATGGCCACTGAGCATATTAGCAATGCTTTCGATTTTCCCGATTAATGAGCGCT	78
QY	61	TTTGGAAATTGACATGATGAAAAACATCCCACTCAAGATGCATACCTCCCTGTAATTTAT	120
Dp	79	TTTGGAAATTGACATGATGAAAAACATCCCACTCAAGATGCATACCTCCCTGTAATTTAT	138
QY	121	GGCATTAATCTTCCTGTTGGGATTTTCCAGGCATATGCAATGATGATATTCACATTATTTTC	180
Dp	139	GGCATTAATCTTCCTGTTGGGATTTTCCAGGCATATGCAATGATGATATTCACATTATTTTC	198
QY	181	AAAATGAAACCTTGGAGAGCAGCAGCAATCATTAATGCTAAACCTGGACGACAGATCTG	240
Dp	199	AAAATGAAACCTTGGAGAGCAGCAGCAATCATTAATGCTAAACCTGGACGACAGATCTG	258
QY	241	CTGATATCTGACCAAGCCTCCCTTCCCTGATTTCACTACTATATGCCAGTGGCGAAAACTGGATC	300
Dp	259	CTGATATCTGACCAAGCCTCCCTTCCCTGATTTCACTACTATATGCCAGTGGCGAAAACTGGATC	318
QY	301	TTTGGAGATTTCAATGATGTAAGTTTATACCGCTCAGCTTCCATTGCAACCTGTAATACAGCT	360
Dp	319	TTTGGAGATTTCAATGATGTAAGTTTATACCGCTCAGCTTCCATTGCAACCTGTAATACAGCT	378
QY	361	ATCCCTCTCCACACTGTGTTTCAGACATCTTCCGCTACTGTGTGATCAATTCACCCAAATGAGC	420
Dp	379	ATCCCTCTCCACACTGTGTTTCAGACATCTTCCGCTACTGTGTGATCAATTCACCCAAATGAGC	438
QY	421	TGCTTTTCATTCACAAAACCTGCATGTGCATGTTTGAAGCTGTGCTGTGCTGTGATGATCATT	480
Dp	439	TGCTTTTCATTCACAAAACCTGCATGTGTGCATGTTTGAAGCTGTGCTGTGCTGTGATGATCATT	498
QY	481	TCACGTGAGCTGATCATTCGATCGATACCTCTTGATACATCAACCAACGAGAACCAACAG	540
Dp	499	TCACGTGAGCTGATCATTCGATCGATACCTCTTGATACATCAACCAACGAGAACCAACAG	558
QY	541	TCAGCCTGTGTCGACCTGACCAAGTTGCGATGGAAGTCAATATCATTTAAGTGTGTAACAACCTA	600
Dp	559	TCAGCCTGTGTCGACCTGACCAAGTTGCGATGGAAGTCAATATCATTTAAGTGTGTAACAACCTA	618
QY	601	ATTTTGATGCGAATCACTTTCTTGCCCTCCCTCGTGATATGTAACACTTTGCTATACACAG	660
Dp	619	ATTTTGATGCGAATCACTTTCTTGCCCTCCCTCGTGATATGTAACACTTTGCTATACACAG	678
QY	661	ATTATATCCACATCTGACCATGATGGAATGCAAACTGCACAGCTGTGTAAGCAAGAAAGCAGCA	720
Dp	679	ATTATATCCACATCTGACCATGATGGAATGCAAACTGCACAGCTGTGTAAGCAAGAAAGCAGCA	738
QY	721	AGGCTAACCAATTCGTGCTACTCCTTGCAATTTTAGTATGTTTATTTTACCTTCATATCTTG	780
Dp	739	AGGCTAACCAATTCGTGCTACTCCTTGCAATTTTAGTATGTTTATTTTACCTTCATATCTTG	798
QY	781	AGGCTCATTTGGATGGAATCTGCGCTGCTTAAATCAGTATGTTTCCATTTAGAAATCAGATC	840
Dp	799	AGGCTCATTTGGATGGAATCTGCGCTGCTTAAATCAGTATGTTTCCATTTAGAAATCAGATC	858
QY	841	CATGAAGCTTACATGCTTTCTAGACACATTAAGCTGCTGTGMAACACCTTGTGTAACCTGTTA	900
Dp	859	CATGAAGCTTACATGCTTTCTAGACACATTAAGCTGCTGTGMAACACCTTGTGTAACCTGTTA	918
QY	901	CTATATGTGTGTGTACGCGACAATTTTACAGCAGGCTGTCTGCTCAACAGTATGATGCAAA	960
Dp	919	CTATATGTGTGTGTGTACGCGACAATTTTACAGCAGGCTGTCTGCTCAACAGTATGATGCAAA	978
QY	961	GTAAAGCGGGAACCTTGAGCAAGCAAGAAATTAATCTTCTCAAAACAACCTCTGA 1014	
Dp	979	GTAAAGCGGGAACCTTGAGCAAGCAAGAAATTAATCTTCTCAAAACAACCTCTCTGA 1032	

AB065877	LOCUS	1414 bp	DNA	linear	PRI 23-JUL-2002
DEFINITION	Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_440.				
ACCESSION	AB065877				
VERSION	AB065877.1 GI:21929018				
KEYWORDS					
SOURCE	Homo sapiens (isolate:CBRC7TM_440) DNA.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S., Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.				
TITLE	Genome-wide discovery and analysis of human seven transmembrane helix receptor genes				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1414)				
AUTHORS	Suwa,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST), 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/, Tel:81-3-3599-8080, Fax:81-3-3599-8081)				
COMMENT	This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding(genedecoder), sequence search, motif-domain assignment and transmembrane helix prediction.				
FEATURES	And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), university of Tokyo].				
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	/db_xref="taxon:9606"				
	/chromosome="13"				
	201..1214				
	/codon_start=1				
	/evidence=not_experimental				
	/product="seven transmembrane helix receptor"				
	/protein_id="BAC06095.1"				
	/db_xref="GI:21929019"				
	/translation="MNEPFLYLANASDFPYPAAFGNCEDENIPLKMYHLYGVIGILF LVGPGAAVVISITYIEKMRPKSSTIIMNLACDILLSLPLIHVYAGSEWING DMQKIFRSPHNLVSLIEFCESIFRGCIVIIHPKSCSIKTRCAVVAACVWIIITLVAVIDPFLITSTNTRNSACIDLTSSBELNTKRYNLILRTATTCLEPLVYITLCY TTIHTLTHGLQTDSCCLKOKARRTIILLAFVYCVLPHILVRIETSLSLISCSIE ENQHEHIVISRPPLAALNTEGNLLVYVSDNFDQAVCSIVRCVSGNLEQAKKISYS NNP"				
ORIGIN	376 a 337 c 260 g 441 t				
Query Match	99.8%; Score 1012.4; DB 9; Length 1414;				
Best Local Similarity	99.9%; Pred. No. 2.3e-257;				
Matches 1013; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
OY	1 ATGAATAGGCACATAGACTATTTTGGCAAAAGCTTCTGATTTCCTCCCGATTATGACAGCTGCT 60				
Db	201 ATGAATAGGCACATAGACTATTTTGGCAAAAGCTTCTGATTTCCTCCCGATTATGACAGCTGCT 260				
OY	61 TTGGAAATTCGACATGATGAAAAACATCCACTCAAGATGACATACCTCCCTGTTATTTAT 120				
Db	261 TTGGAAATTCGACATGATGAAAAACATCCACTCAAGATGACATACCTCCCTGTTATTTAT 320				
OY	121 GGCAATTATCTTCTCGTGGGATTTCCACGGCAATGACATAGTGAATATCCACTTACATTTTC 180				
Db	321 GGCAATTATCTTCTCGTGGGATTTCCACGGCAATGACATAGTGAATATCCACTTACATTTTC 380				

QY 181 AAAATGAGACCTTGGAGAGACAGACCATATTATGCTGAACCTGGCCCTGCAGACTCTG 240
 DB 381 AAAATGAGACCTTGGAGAGACAGACCATATTATGCTGAACCTGGCCCTGCAGACTCTG 440
 QY 241 CCGTATCTGACAGAGCTCCCTTCTGATTCACCTACTATGACAGTGGGCAAACTGGATC 300
 DB 441 CCGTATCTGACAGAGCTCCCTTCTGATTCACCTACTATGACAGTGGGCAAACTGGATC 500
 QY 301 TTGGAGATTTATGATGATGATTTATCCGCTCAGCTTCATTTCAACTGATATGACAG 360
 DB 501 TTGGAGATTTATGATGATGATTTATCCGCTCAGCTTCATTTCAACTGATATGACAG 560
 QY 361 ATCCCTTCCTCAGCTGTTTACAGCATCTTCGCTACTGATGATCATTCACCAATGAGC 420
 DB 561 ATCCCTTCCTCAGCTGTTTACAGCATCTTCGCTACTGATGATCATTCACCAATGAGC 620
 QY 421 TGCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 621 TGCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 680
 QY 481 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 681 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
 QY 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 741 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
 QY 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 801 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
 QY 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 861 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 920
 QY 721 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 921 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
 QY 781 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 981 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1040
 QY 841 CATGAAGCTTACATGCTTCTGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 1041 CATGAAGCTTACATGCTTCTGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1100
 QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 1101 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
 QY 961 GTPAGCGGAGACCTTGGAG 1014
 DB 1161 GTPAGCGGAGACCTTGGAG 1214

RESULT 11
 AX379470 9905 bp DNA linear PAT 18-MAR-2002
 LOCUS AX379470 Sequence 3 from Patent WO0187980.
 DEFINITION AX379470
 ACCESSION AX379470
 VERSION AX379470.1 GI:19575227
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 Wei, M.H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and
 Beasley, E.M.
 TITLE
 Isolated human g-protein coupled receptors, nucleic acid molecules
 encoding human gper proteins, and uses thereof

JOURNAL Patent: WO 0187980-A 3 22-NOV-2001;
 Applera Corporation Robert A. Millman Assistant Secretary (us)
 FEATURES Location/Qualifiers
 Source 1..9905
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 2656 a 2218 c 2061 g 2970 t
 ORIGIN
 Query Match 99.8%; Score 1012.4; DB 6; Length 9905;
 Best Local Similarity: 99.9%; Pred. No. 2.5e-257;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGAATGAGACCTTGGAGAGACAGACCATATTATGCTGAACCTGGCCCTGCAGACTCTG 60
 DB 8309 ATGAATGAGACCTTGGAGAGACAGACCATATTATGCTGAACCTGGCCCTGCAGACTCTG 8368
 QY 61 TTGGAAATGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 DB 8369 TTGGAAATGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8428
 QY 121 GGCATTATCTCTCTGCTGGGATTTCCAGGCAATGCGATGATGATGATGATGATGATGATGAT 180
 DB 8429 GGCATTATCTCTCTGCTGGGATTTCCAGGCAATGCGATGATGATGATGATGATGATGATGAT 8488
 QY 181 AAAATGAGACCTTGGAGAGACAGACCATATTATGCTGAACCTGGCCCTGCAGACTCTG 240
 DB 8489 AAAATGAGACCTTGGAGAGACAGACCATATTATGCTGAACCTGGCCCTGCAGACTCTG 8548
 QY 241 CCGTATCTGACAGAGCTCCCTTCTGATTCACCTACTATGACAGTGGGCAAACTGGATC 300
 DB 8549 CCGTATCTGACAGAGCTCCCTTCTGATTCACCTACTATGACAGTGGGCAAACTGGATC 8608
 QY 301 TTGGAGATTTATGATGATGATTTATCCGCTCAGCTTCATTTCAACTGATATGACAG 360
 DB 8609 TTGGAGATTTATGATGATGATTTATCCGCTCAGCTTCATTTCAACTGATATGACAG 8668
 QY 361 ATCCCTTCCTCAGCTGTTTACAGCATCTTCGCTACTGATGATCATTCACCAATGAGC 420
 DB 8669 ATCCCTTCCTCAGCTGTTTACAGCATCTTCGCTACTGATGATCATTCACCAATGAGC 8728
 QY 421 TGCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 8729 TGCCTTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 8788
 QY 481 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 8789 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8848
 QY 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 8849 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8908
 QY 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 DB 8909 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8968
 QY 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 8969 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9028
 QY 721 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 9029 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9088
 QY 781 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 9089 AGGCTAAGCAATCTGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9148
 QY 841 CATGAAGCTTACATGCTTCTGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 9149 CATGAAGCTTACATGCTTCTGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9208

QY 901 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGGCTGTCTCTCAACAGTATGATGCAA 960
Db 9209 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGGCTGTCTCTCAACAGTATGATGCAA 9268
QY 961 GTAGCGGGAACCTTGAGCAAGCAAAATGTTACTTCAACACCCCTTGA 1014
Db 9269 GTAGCGGGAACCTTGAGCAAGCAAAATGTTACTTCAACACCCCTTGA 9322

RESULT 12
AL356486/c 67645 bp DNA linear PRI 28-SEP-2001
LOCUS Human DNA sequence from clone RP11-721F14 on chromosome 13,
DEFINITION complete sequence.
ACCESSION AL356486
VERSION AL356486.12 GI:15808158
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 67645)
AUTHORS Skuce, C.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Sep 28, 2001 this sequence version replaced gi:15808158.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone confis of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-721F14 is from the library RPII-11.3 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/dacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-721F14. It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-19817 is at 65646 in this
sequence. The true right end of clone RP11-65119 is at 2000 in this
sequence.

FEATURES
Source
1. 67645
/organism="Homo sapiens"
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/chromosome="13"
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/clone_id="RPII-11.3"
misc_feature
53919
/note="Tandem repeat. Forced join. Gap size estimated to
be approximately 110bp by restriction digest. data."
BASE COUNT 20542 a 13252 c 13216 g 20635 t
ORIGIN

Query Match 99.8%; Score 1012.4; DB 9; Length 67645;
Best Local Similarity 99.9%; Pred. No. 2.7e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAGCAGCAGTATTTAGCAATGCTTCTGTATTTCCCGATTTAGAGCTGCT 60
Db 5091 ATGATGAGCAGCAGTATTTAGCAATGCTTCTGTATTTCCCGATTTAGAGCTGCT 5032
QY 61 TTGGAAATTCAGTATGAAATATCCCACTCAAGATGACACTACCTCCCTGATTTAT 120
Db 5031 TTGGAAATTCAGTATGAAATATCCCACTCAAGATGACACTACCTCCCTGATTTAT 4972
QY 121 GGCAATATCTTCTCTGTTGGATTTCCAGCAATGACAGTATGATATCCACTTAT 180
Db 4971 GGCAATATCTTCTCTGTTGGATTTCCAGCAATGACAGTATGATATCCACTTAT 4912
QY 181 AAAATGAGACTTTGGAAGAGAGAGACCATATTTGCTGAACCTGGGCTGCAGAGATCTG 240
Db 4911 AAAATGAGACTTTGGAAGAGAGAGACCATATTTGCTGAACCTGGGCTGCAGAGATCTG 4852
QY 241 CTGTATCTGACAGCAGCTCCCTCTGATTCAGTATGAGAGAGAGAGAGAGAGATC 300
Db 4851 CTGTATCTGACAGCAGCTCCCTCTGATTCAGTATGAGAGAGAGAGAGAGAGATC 4792
QY 301 TTGGAGATTTGATGTATGATTTATCCGCTTCAGCTTCATTTCAACTGTATAGCAGC 360
Db 4791 TTGGAGATTTGATGTATGATTTATCCGCTTCAGCTTCATTTCAACTGTATAGCAGC 4732
QY 361 ATCCCTCTTCCAGCAGCTGTTTCAGATCTCCGCTGCTGATGATTTCAACCAATAGC 420
Db 4731 ATCCCTCTTCCAGCAGCTGTTTCAGATCTCCGCTGCTGATGATTTCAACCAATAGC 4672
QY 421 TGCCTTTTCATTCACAAACATCGATGTGAGTTGATGCTGCTGCTGCTGATGAT 480
Db 4671 TGCCTTTTCATTCACAAACATCGATGTGAGTTGATGCTGCTGCTGATGAT 4612
QY 481 TCATGTTAGCTGTATTCGAGTACCTCTTGTATCATATCAACCAAGAGACCAAGAG 540
Db 4611 TCATGTTAGCTGTATTCGAGTACCTCTTGTATCATATCAACCAAGAGACCAAGAG 4552
QY 541 TCACCTGCTGCGACGTCACAGTGGAGTGAATCAATCAATTAAGTGGTCAACCTA 600
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Db 4491 ATTTGAGCTGCAATCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4432
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Db 4431 ATATTCACACTGTGACCCATGACGCTGCAACAGTACGCTGCTGCTGCTGCTGCT 4372
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Db 4371 AGGCTACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4312
QY 781 AGGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 4311 AGGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4252
QY 841 CATGACCTTACATGCTTTCTGATGACATGATGCTGCTGATGACATGCTGCTGAT 900
Db 4251 CATGACCTTACATGCTTTCTGATGACATGATGCTGCTGATGACATGCTGCTGAT 4192
QY 901 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGGCTGTCTCTCAACAGTATGATGCAA 960
Db 4191 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGGCTGTCTCTCAACAGTATGATGCAA 4132
QY 961 GTAGCGGGAACCTTGAGCAAGCAAAATGTTACTTCAACACCCCTTGA 1014
Db 4131 GTAGCGGGAACCTTGAGCAAGCAAAATGTTACTTCAACACCCCTTGA 4078

RESULT 13
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LOCUS AC026756
DEFINITION Homo sapiens chromosome 13 clone RP11-286P8, complete sequence.
ACCESSION AC026756
VERSION AC026756.15 GI:13112251
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedorispiet,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
Yu,S. and Davis,R.W.
JOURNAL Unpublished
REFERENCE
AUTHORS 2 (bases 1 to 156555)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedorispiet,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
JOURNAL Direct Submission
TITLE Submitted (23-MAR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
REFERENCE
AUTHORS 3 (bases 1 to 156555)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedorispiet,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Lam,B., Mao,J., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
Yu,S. and Davis,R.W.
JOURNAL Direct Submission
TITLE Submitted (23-FEB-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT
On Feb 23, 2001 this sequence version replaced gi:12745089.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDBTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 870
Center clone name: RP11-286P8

----- Summary
This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
Location/Qualifiers
source
1. 156555
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-286P8"
/clone_1lb="RPC1 human BAC library 11"
BASE COUNT 48748 a 30845 c 30755 g 46207 t
ORIGIN
Query Match 99.8%; Score 1012.4; DB 9; Length 156555;
Best Local Similarity 99.9%; Pred. No. 2.7e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGATGAGGCACCTGACATTTACCAATGCTTCGATTCCCGCATATATGAGCTGCT 60
|||||
140188 ATGAATGAGGCACCTGACATTTACCAATGCTTCGATTCCCGCATATATGAGCTGCT 140247

OY		61	TTTTGAAATTTGCACGTAGTGAAGAAAACAATCCACCACACAGATGACACTACCTCCCTGGATTATTA	120
Dd		140248	TTTGGAATTTTGACAGTAGATGAATAAACAATCCACACAGATGACACTACCTCCCTGGATTATTA	140307
OY		121	GGCATTATCTTCCTCGTGGGATTTTCCAGGCCAAATGCAATGAGTAGTGATATCCATTACATTTTC	180
Dd		140308	GGCATTATCTTCCTCGTGGGATTTTCCAGGCCAAATGCAATGAGTAGTGATATCCATTACATTTTC	140366
OY		181	AAAAATGAGACCTTGGAGAAGACAGCACACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG	240
Dd		140368	AAAAATGAGACCTTGGAGAAGACAGCACACCATCATTTATGCTGAACCTGGCCTGCACAGATCTG	140427
OY		241	CTGTATCTGACAGGCTCCCCCTCCGATTACTACTATAGCCAGTGGGCGAAAACTGGATTC	300
Dd		140428	CTGTATCTGACAGGCTCCCCCTCCGATTACTACTATAGCCAGTGGGCGAAAACTGGATTC	140487
OY		301	TTTGGAGATTTTCATGTGTATGATTTATTCGCTTCAGCTTCATTTCAACCTGTATTAGCAGC	360
Dd		140488	TTTGGAGATTTTCATGTGTATGATTTATTCGCTTCAGCTTCATTTCAACCTGTATTAGCAGC	140544
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VERSION	AXI191332.1	GI:15209582		
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Glucksmann, M.A. and White, D.
TITLE 26904, 38911, and 39404, seven-transmembrane proteins / g-protein coupled receptors
JOURNAL Patient: WO 0149847-A 2 12-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
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LOCUS AX147840
DEFINITION Sequence 85 from Patent WO0136473.
ACCESSION AX147840
VERSION AX147840.1 GI:14346841
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Vogel, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kayles, P.S., Bannigan, C.M., Ruff, V., Sejlitz, T., and Huff, R.M.
TITLE Novel g protein-coupled receptors
JOURNAL Patient: WO 0136473-A 85 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:40:53 ; Search time 81 Seconds
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Title: US-10-023-775B-2
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0
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Listing first 45 summaries

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2: sp_bacteria:*
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4: sp_human:*
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8: sp_organelle:*
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15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	556.5	31.4	361	13	Q90X57
4	547	30.9	374	13	Q57466
5	479	27.0	330	4	Q9BXA5
6	479	27.0	334	4	Q9BXA5
7	445.5	25.2	309	11	Q8R528
8	421	23.8	328	11	Q8R528
9	418	23.6	317	11	Q9ERK9
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ALIGNMENTS

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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
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GN GPR80 OR GPCR.
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RX MEDLINE-21458557; PubMed-11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arhltko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411109; AL26480.1; -;
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DR InterPro: IPR000276; GPCR_Kinopsn.
DR Pfam: PF00001; 7tm_1; 1.
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SQ SEQUENCE 337 AA; 38251 MW; 6814EA0044756CE6 CRC64;
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DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P2Y receptor.
OS Raja erinacea (little skate).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hyposqualae; Pristigastera; Batoidae;
OC Rajiformes; Rajidae; Raja.
OC NCBI_TaxID=7782;
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RC TISSUE=LIVER.
RX MEDLINE=20459151; PubMed=10900200;
RA Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Connolly G.C.,
RA Ballatori N., Boyer J.L., Nathanson M.H.;
RT "A primitive ATP receptor from the little skate Raja erinacea."
RL J. Biol. Chem. 275:30701-30706(2000).
DR EMBL: AF242850; AAC42684.1;
DR HSSP: P34996; 1DDO.
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DR Pfam: PF00001; 7tm_1; 1.
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RESULT 3

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AC 090X57;
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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8353;
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RP SEQUENCE FROM N.A.
RA Cheng A.W., Tsai K.W.;
RT "Cloning of Xenopus P2Y1 Receptor."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF432354; AAL27614.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR NCBI_MolMap: M00001;
SQ SEQUENCE 361 AA; 41002 MW; E5B2D605F5B57BED CRC64;
```

Query Match 31.4%; Score 556.5; DB 13; Length 361;
Best Local Similarity 35.2%; Pred. No. 1.4e-44;
Matches 113; Conservative 70; Mismatches 123; Indels 15; Gaps 4;

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QY 22 GN--CNDENIPKMHYLPVYIGIIFLVGPGNAVISTYIFKMRPKSSTIMLACT 78
Db 25 GNVTKCILTGTGFOFYLPVYIYVCTGTGNSVALMTFHKRPMSSISVYMFNIALA 84
QY 79 DLVLTSLPLIHYASGEMWIGDMCKFIRSFHNLYSSILFLTCFSIFRYCVIIHP 138
Db 85 DLVLTSLPLIHYASGEMWIGDMCKFIRSFHNLYSSILFLTCFSIFRYCVIIHP 144
QY 139 MSCFSIHKTRCAVAVCAVWIISLVAVIPMTFLTSTNTRNS-ACIDLTSDELNTIK 197
Db 145 LKSLGRKKRKNISYISALVWFYIAGISPLIFSGTGRKKTKTCFDTSSDEYLRSYFI 204
QY 198 YNLIILPTATTCPLVITLTCTTIIHILHTGLQDSCLOKARLTILLAFYVCLPF 257
Db 205 YSMCTTVFGCIPILILGCGYGLVRLIKDMNNAFLRKRSYIVITVIVAVASLPLF 264
QY 258 HILVIRIESRLSISCSINQIHEAVISRPALALMTFGNLIVVVSDNFQAVC 314
Db 265 HVKKNLRLRLDQSPKCNFNDRVYATQVIRGLASLNSCVDPILYFLAGDIF----- 319
QY 315 STVRCVSGNLEQAKKISYSN 335
Db 320 ---RRKLSRATWRKASRSEAN 337
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RESULT 4

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ID 057466 PRELIMINARY; PRT; 374 AA.
AC 057466;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
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DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE G-protein coupled P2Y nucleotide receptor.
 GN TP2Y.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood.
 RX MEDLINE=98086419; PubMed=9415702;
 RA Boyer J.L., Waldo G.L., Harden T.K.;
 RT "Molecular cloning and expression of an avian G-protein-coupled P2Y
 receptor."
 RL Mol. Pharmacol. 53:928-934(1997).
 DR EMBL: AF031897; AAC60339.1; -.
 DR HSSP: P34996; 1DD.
 DR InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 374 AA; 42594 MW; 849C465722BD02B CRC64;
 Query Match 30.9%; Score 547; DB 13; Length 374;
 Best local Similarity 36.2%; Pred. No. 1,le-43;
 Matches 108; Conservative 62; Mismatches 122; Indels 6; Gaps 3;
 QY 18 AAAGNCTDENIPDKMHLVPIYIGIFLVGPGNAVVISYIFKMRPMKSSITIMNLAC 77
 DB 27 AAAGACV-FNEEFKILLPISYIGIFLVGPGNAVVISYIFKMRPMKSSITIMNLAC 85
 QY 78 TDLLVLTSLPFLIHVYASGENMTFGDMCKFIRSFHNLSSILFLTCFIRYCVI 137
 DB 86 SDLVVSLPFLVYADRNMPFGKVFCKIVFELFVYANLYSSILFLTCISVHRMGICH 145
 QY 138 PMSCFSIHKTCAVAVCAVWVWISLVAVIMPTLITSTNTRNSACIDLTSSDELNTIKW 197
 DB 146 PIRSLKWKTKHARLKCQVGLVVTICLIPNLFLVTTSSNDNTLCHDTKPREPFIYVH 205
 QY 198 YNLTATPFCPLVITVLYTCYTTIHTL-THGLQDTS---CIKQARRLTILLAFVY 252
 DB 206 YSSISALLFGIFLIVYVCICMAKRLCKRSEPSRPSVYKRSIKMIITLVTFAL 265
 QY 253 CPEFHILVIRIESNLSISCSIEINOIHAYIVSRPLALNFGNLLVYVSDNFQ 310
 DB 266 CPEFHITRTLYTSRYPQADCOITLINTFYKITRPLASINSCLDPIYFMAGDYR 323
 RESULT 5
 Q9BXA5 PRELIMINARY; PRT; 330 AA.
 AC Q9BXA5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE G-protein coupled receptor 91.
 GN GPR91.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21172992; PubMed=11273702;
 RA Mittenberger T., Schaller H.C., Heilebrand S.;
 RT "An expressed sequence tag (est) data mining strategy succeeding in
 the discovery of new G-protein coupled receptors."
 RL J. Mol. Biol. 307:799-813(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF348078; AAK29080.1; -

DR HSSP: P34996; 1DD.
 DR InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 330 AA; 38283 MW; 6D3C70E340866BAB CRC64;
 Query Match 27.0%; Score 479; DB 4; Length 330;
 Best local Similarity 35.9%; Pred. No. 2,7e-37;
 Matches 110; Conservative 61; Mismatches 123; Indels 12; Gaps 6;
 QY 23 NCTDEN-----IFLKMHLVPIYIGIFLVGPGNAVVISYIFKMRPMKSSITIMNLAC 77
 DB 4 NATCKMMLAAEALDEKTYISIFGIEFVGLNTIVYGYISLKMNSNNTIYFLVSLV 63
 QY 78 TDLLVLTSLPFLIHVYASGENMTFGDMCKFIRSFHNLSSILFLTCFIRYCVI 137
 DB 64 SDLAFLCTLPMLIRSYANG-NWLYGDLICISNRVYLANLYTSLFLTFISIDRYLIRY 122
 QY 138 PMSCFSIHKTCAVAVCAVWVWISLVAVIMPTLITSTNTRNSACIDLTSSDELNTIKW 197
 DB 123 PFREHLQKKEFAILLISLAIWLVLTLEPLIPLIPVITDNGTCNDFASSGDPVYNTLI 182
 QY 198 YNLTATPFCPLVITVLYTCYTTI-ITHTHGLQDTSCK-QKARRLTILLAFVYCF 255
 DB 183 YSMCLILLGLFLIPFMCFFYKYALFLKORNOVATLPLEPMLINAVYIFSVLFT 242
 QY 256 PFHILVIRIESNLS--ISCSIEINOIHAYIVSRPLALNFGNLLVYVSDNFQ 312
 DB 243 PYHVMNRVIRASLSGKQYCT-QVYINSFYITRPLAFINSVINPVEYFLGDHFRDM 301
 QY 313 VCSTVR 318
 DB 302 LNMQLR 307
 RESULT 6
 O8TD08 PRELIMINARY; PRT; 334 AA.
 ID O8TD08;
 AC O8TD08;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE P2Y purinoceptor 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Li N., Wan T., Cao X.;
 RT "Human P2Y purinoceptor 1."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF247785; AAL95690.1; -.
 SQ SEQUENCE 334 AA; 38697 MW; 33146ELAD87F0E81 CRC64;
 Query Match 27.0%; Score 479; DB 4; Length 334;
 Best local Similarity 35.9%; Pred. No. 2,7e-37;
 Matches 110; Conservative 61; Mismatches 123; Indels 12; Gaps 6;
 QY 23 NCTDEN-----IFLKMHLVPIYIGIFLVGPGNAVVISYIFKMRPMKSSITIMNLAC 77
 DB 8 NATCKMMLAAEALDEKTYISIFGIEFVGLNTIVYGYISLKMNSNNTIYFLVSLV 67
 QY 78 TDLLVLTSLPFLIHVYASGENMTFGDMCKFIRSFHNLSSILFLTCFIRYCVI 137
 DB 68 SDLAFLCTLPMLIRSYANG-NWLYGDLICISNRVYLANLYTSLFLTFISIDRYLIRY 126
 QY 138 PMSCFSIHKTCAVAVCAVWVWISLVAVIMPTLITSTNTRNSACIDLTSSDELNTIKW 197
 DB 127 PFREHLQKKEFAILLISLAIWLVLTLEPLIPLIPVITDNGTCNDFASSGDPVYNTLI 186

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QY 198 YNLTATTCPLPVIVTCTTT-ITHLHGLQFDSCLK-QKARRLTLLLLAFYVCF 255
D 187 YSMCLTTLGLFLPLFVWCFYKIALFLKONROVAATLPEKLNLTIVMAVVFSLFT 246
QY 256 PFHLIRVIRIESRLS---ISCSTENOIHEAVIYSRPLAINTFENLLVYVSDNQQA 312
D 247 PYHVMRWRIASRLSGWKXOCT-QVINSFYIVTRPLAFINSYINPFVFLGDHFRDM 305
QY 313 VCSFVR 318
D 306 LAMOLR 311

RESULT 7
08R528 PRELIMINARY; PRT: 309 AA.
AC 08R528;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cysteinyl leukotriene 2 receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishii S.;
RT "Mouse Cyslt2 Gene.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB058930; BAB86881.1; -.
KW Receptor.
SQ SEQUENCE 309 AA; 35226 MW; 96FACC68BAF96974 CRC64;

Query Match 25.2%; Score 445.5; DB 11; Length 309;
Best Local Similarity 33.6%; Pred. No. 3.8e-34;
Matches 102; Conservative 61; Mismatches 122; Indels 19; Gaps 10;

QY 23 NCTDENIPLMHYPLVYIGIIFLVGPGNNAVISTYIFKMRPKSST---IIMNLACTD 79
D 14 NCTIEN--FKKEPIIYLIIFEGALGNG--FSIYF-IQTCRKSISVNMFMNLATSD 68
QY 80 LLYTSLPFLIHYAASENMIFGDMCKFRFSFHNLYSSILFLCFISFRVCVTHPM 139
D 69 FLFSLPLFRADYFRSGNMIFGDLACRVSYSILYVMYTSIYFLYLSVFRFLAHPF 128
QY 140 SCFISHTRCVAVACAVWIIISIVAVIPMFELISTRTNSACLDLTSSDELTIKYN 199
D 129 RMFVITSVRSAMWLCGIWVF-IMASSALLVNGQEEKDNITISLEL-SPKFRSLIMN 186
QY 200 LILTATTCPLPVIVTCTTT-ITHLHGLQFDSC---CLKOKARRLTLLLLAFYVCF 256
D 187 HIAVAVGFLPLFLTFLTCYLLIRILTKAEIPESGPRARHKALTIVIAMITFLCLFP 246
QY 257 PHILIRVIRIESRLSICSTENOIHEAVIYSRPLAINTFENLLVYVSDNQ--QAV 313
D 247 YHMLRTHLVY-MDKDSCG--DVLKAKATVITLFWAANSCFNPLLYFAGENFKAIRAI 303
QY 314 CSFY 317
D 304 FSKY 307

RESULT 8
09ERK9 PRELIMINARY; PRT: 328 AA.
AC 09ERK9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE p3y6 receptor (Hypothetical 36.7 kDa protein).
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-129/SVEV;
RC STRAIN-129/SVEV;
RX MEDLINE=21160052; PubMed=11259526;
RA Lazarowski E.R., Rochelle L.G., O'Neal M.K., Ribeiro C.M.P.,
Grubb B.R., Zhang V., Harden T.K., Boucher R.C.;
RT "Cloning and functional characterization of two murine uridine
nucleotide receptors reveal a potential target for correcting ion
transport deficiency in cystic fibrosis gallbladder.";
RL J. Pharmacol. Exp. Ther. 297:43-49(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298899; AAC24619.1; -.
DR EMBL; BC027331; AAH27331.1; -.
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Hypothetical protein; Receptor.
SQ SEQUENCE 328 AA; 36721 MW; 00F9DF5ADADF903E CRC64;

Query Match 23.8%; Score 421; DB 11; Length 328;
Best Local Similarity 32.9%; Pred. No. 8.3e-32;
Matches 96; Conservative 45; Mismatches 125; Indels 26; Gaps 5;

QY 36 LPVYIGIIFLVGPGNNAVISTYIFKMRPKSSTIIMNLACTDLVLTSLPFLIHYAS 95
D 29 LTPYSVLVVGLPLNCIVAIQICASRRTLTRSAVYTLNLADLMTACSLPLIYVAR 88
QY 96 GEMNIFGDMCKFRFSFHNLYSSILFLCFISFRVCVTHPMSCSIRK---TRAVY 152
D 89 GDHMPFDLACRFVRFLEYANLHGSILFLTCISFORYLGICHPLA--SMNRGGGRAAW 146
QY 153 ACVAVWIIISIVAVIPMFELISTRTNSACLDLTSSDELTIKYNLITATTCPLV 212
D 147 VCGVWVLAIVAOCLPTAVFAATGIGORNRVCYDLSPIILSTRYPGMALTVIGFLPFI 206
QY 213 IVTLCTYTTIHTLHGLQDSC-----LKOKARRLTLLLLAFYVCFPLPHIL 260
D 207 ALLACCYRMARL-----CRQDGPAPVAGQERSKAAMAVVAVPAISPLPHIT 258
QY 261 RVIIIESRL-SICSTENOIHEAVIYSRPLAINTFENLLVYVSDNQ 311
D 259 KTAVLAVRSTPGVSCPVLTFPAAYKGTTPRASVNSVLDPLTFYEQKFR 310

RESULT 9
09MT6 PRELIMINARY; PRT: 317 AA.
AC 09MT6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G-protein coupled receptor GPR91.
GN GPR91.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL;
RC STRAIN-C57BL;
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebren S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
the discovery of new g-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).

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DR EMBL: AF295367; AAK01867.1; -
 DR HSSP: P34996; 1DD.
 DR MGD: MG1:1934135; GP-9L.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_F1_2; 1.
 KW Receptor.

SO SEQUENCE 317 AA; 36701 MW; 4E22F0608F92B836 CRC64;

Query Match 23.6%; Score 418; DB 11; Length 317;
 Best local Similarity 33.7%; Pred. No. 1.5e-31;
 Matches 99; Conservative 58; Mismatches 127; Indels 10; Gaps 6;

QY 31 LKMHLPVYIGIIFLVGFGNAVISTYIFKMRPKSSITIMLNLACTDLYLTSPLFI 90
 DB 17 LKRYLSAFYAEFEFGLGNVTYVGYLFCKMKNSSNVYLENLSISDFAEFLCTPLFI 76
 QY 91 HYVASENMFQDFMCKFRFSFHFNLVSSILFLCFISIRYCVIIHPMSCFSIHKTCA 150
 DB 77 KRYAN-DKGTGADVLCISNRIVLHNLITSMILLIYISMDRIIMKYPFRHFLQKKEFA 135
 QY 151 VVACAVWIIISLVAVIPMTFLITSNRTNRSAICDLTSS--DELTIKWYNLITATTEC 208
 DB 136 ILISLAVMLVTLVPLMTFLITSVYKKEGSCNIDYASSGNPEHNL--YSICLTLGLFL 193
 QY 209 LPLVIVTLCYTIITHTLHGLQDSC--KOKARLTILLALFYCFLPHILVRIE 266
 DB 194 IFLVWCFEYKRVVFLKRRSQQAFLPLDKPRLVAVIVFSLFPTPYHMRMLRIA 253
 QY 267 SRLLS--ISCSIEINOHEAVYSRPLAALNTFGNLLVYVSDNQOAVCSYVR 318
 DB 254 SRLDSWPGOCT-QKAIKSYITLIRPLAFINSALNPLFTYLMGDHTEMILSKFR 306

RESULT 10
 QY0006 PRELIMINARY; PRT; 369 AA.

AC QY0006; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Chemokine receptor CCR9 (CC chemokine receptor 9A).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9248139; PubMed-10229797;
 RA Zabaillo A., Gutierrez J., Varona R., Ardañiz C., Marquez G.,
 RT Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
 RT receptor for the chemokine TECK.
 RL J. Immunol. 162:5671-5675(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yu C.-R., Peden K.W.C., Farber J.M.,
 RT "CCRB and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/CXCR6-
 RT 15)."
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: A133337; CAB43477.1; -
 DR EMBL: AF145439; AAF66699.1; -
 DR InterPro: IPR004069; CC_Chemkin9.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR01558; CHEMOKINER1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_F1_2; 1.
 KW Receptor.

SO SEQUENCE 369 AA; 42015 MW; F27CEA0CFB6844C CRC64;

Query Match 22.5%; Score 399; DB 4; Length 369;
 Best local Similarity 29.1%; Pred. No. 1.1e-29;
 Matches 104; Conservative 70; Mismatches 145; Indels 38; Gaps 11;

QY 4 PLDYLANASDFPDYAAAFGN-----CTDENI-PLKMHLPVYIGI 44
 DB 3 PDIFF---TSPTRMADYSESTSSMEDVYVNFDFYCKNNVRGFAHFPLPLXWLV 59
 QY 45 LVGFPNAVISTYIFKMRPKSSITIMLNLACTDLYLTSPLFIHYVASENMFQDF 104
 DB 60 IYAGLNSIVILVYVWCTRYKMTDMFLNLALADLFLVTLPLFMA--IAADQWQFQF 117
 QY 105 MCKFRFSFHFNLVSSILFLCFISIRYCVIIHPMSCFSIHKTCA--AVACAVWIIISL 162
 DB 118 MCKVNSMKMKNFSCVLLIMKISVDYVIAIQAMAHARWREKRLYSKMGVFTIWLVA 177
 QY 163 VAVIPMTFLITSNRTNRSAICDLTSSDELTIKWYNLITATTE--FCLPLVIVTLCY 219
 DB 178 ALCIPEILXSQKESGIALCMVYPSDESTK--SAVLTILVILGFLPLPYVMACCT 235
 QY 220 TIIHTLHGLQDSCIKOKARLTILLALFYCFLPH-ILVRIESRLSIS-CSIE 277
 DB 236 IITHTL---IOAKSSKHKALKVTLVTLVFLVLSOPRYNCILLVOTIDYAMFISNCAVS 292
 QY 278 NOIHEAVYSRPLAALNTFGNLLVYVSDNQOAVCSYVRVCSNGLQAKKISVS 334
 DB 293 TINDICEOYVOTIAFHSCNPLVYVGERFRDLVKT--KNIGCSIQAOQWVSPT 347

RESULT 11
 QY0R311 PRELIMINARY; PRT; 399 AA.

AC QY0R311; 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
 DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Coagulation factor II (thrombin) receptor-like 1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.,
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC025432; AAH25432.1; -
 KW Receptor.

SO SEQUENCE 399 AA; 44679 MW; 807C79464AB9B3EF CRC64;

Query Match 22.0%; Score 390.5; DB 11; Length 399;
 Best local Similarity 29.9%; Pred. No. 7.6e-29;
 Matches 97; Conservative 65; Mismatches 129; Indels 33; Gaps 9;

QY 35 YLPVYIGIIFLVGFGNAVISTYIFKMRPKSSITIMLNLACTDLYLTSPLFIHYA 94
 DB 79 FLPVVITIVFVGLPSNGMALWFLRTKKHDPVIVMANLADLSVTFPLATAYHL 138
 QY 95 SEENMFQDFMCKFRFSFHFNLVSSILFLCFISIRYCVIIHPMSCFSIHKTCAVAVAC 154
 DB 139 HGNMNVYAGALCKVLGFFYGNMNYCSILMTCLSVGRVAVYNPQG---HRRKANIV 194
 QY 155 AV---VWISLVAVIPM-----TFLITSNRTNRSAICDLTSSDEL-NTIKWYNLITAT 205
 DB 195 GVSALWMLFLVTLPIVLYWKOTIYIPALNIT---TCHVLPDEVLVGMFVFLSLAG 251
 QY 206 TFCPLVIVTLCYTIITHTLHGLQDSC--KOKARLTILLALFYCFLPHILVRIE 263
 DB 252 VFLFPAITLAVSAVILKTLRSSADHSEKRRORIRLITVLAIFYCFAPSNLILV 311
 QY 264 RIESRLSISCSIEINOHEAVYSRPLAALNTFGNLLVYVSDNQO-----AVCSYVR 318

Db 312 ----HFLLITQROSHVAYLYALALCLSTLNSCIDPVIYFVSKDFDHANALLCSVR 367
 QY 319 -----CKVSGNLEQAKKISYSNN 336
 Db 368 TVNMQISTLSNKRKSGSSSS 391

RESULT 12

Q90222 PRELIMINARY; PRT; 359 AA.
 AC Q90222;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE IL-8 receptor.
 GN IL-8.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang H., Thorngard G.H., Ristow S.S.;
 RT "Molecular cloning and genomic structure of an interleukin-8 receptor-
 like gene from a homozygous clones of rainbow trout (Oncorhynchus
 mykiss).";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF260964; AK48500.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_FL2; 1.
 KM Receptor.
 SQ SEQUENCE 359 AA; 39981 MW; A92A9038AAC97B7B CRC64;

Query Match 20.8%; Score 369; DB 13; Length 359;
 Best Local Similarity 30.3%; Pred. No. 7.5e-27;
 Matches 105; Conservative 62; Mismatches 136; Indels 44; Gaps 13;

QY 1 MNEPLDYLANASDPDYAAA-----FGNCTDENI-----PLKMHYLPVIGII 43
 Db 1 MFEVLIDYDKA-DY-DYKSNDSYFRTSFDLNFDLISCAQPLSGAVIFLCVLAIV 58
 QY 44 FLVGFEGNAVITYITFKMRPKMSSTIMLNACTDILYLTSLPELIHYASG--ENWIF 101
 Db 59 FLTAVGNTLVGLVIGFSQOSLTPSDVYLFHLTVADGLALTLPF---WAAMTIGHMIF 114
 QY 102 GDMCKFRIRSFHFNYSILFLCPSIFRYCVIIMHSCFSIHKTCAVAVACAVVITIS 161
 Db 115 GDLCKRFLSLVMEASEFTSLFLVCLSDRYLVIVRPKSRKGRACRMVACTFTWTLG 174
 QY 162 LVAVIEMTFLITST-NRTNSAC---DLTSSD--ELNTIKWNLITATFCLPIVIY 215
 Db 175 GALSPLALFMDATPQGGPTPCAHEHDDLSATHWRATGLRIIL-----GFLPLVIMV 230
 QY 216 LCYTTIIHIL--THGLQDSCLOKARRLTILLAAVYCFLEPH--ILVIRIESPLLS 271
 Db 231 ACYSIVVARLLQTHGEF-----KHRAKRVIIIAVFAFLLCWTFPLHMTVADTLIRAKLV 285
 QY 272 ISGSIHQHEATIVSRPLAANTFGLLLYVVSNDPQAVCSIVR 318
 Db 286 FDCAVNRVDLALQVTHSLALVHSFVPLVYAFVGEKFRGNLALVR 332

RESULT 13

Q9NOM0 PRELIMINARY; PRT; 358 AA.
 AC Q9NOM0;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE GCR3 receptor.

OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wolfe G.C., Mudgett J.S.;
 RT "Cloning and characterization of the sheep GCR3 receptor."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF265468; AAF71786.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_FL2; 1.
 KM Receptor.
 SQ SEQUENCE 358 AA; 40985 MW; 2B54F9128590181E CRC64;

Query Match 20.3%; Score 359.5; DB 6; Length 358;
 Best Local Similarity 28.2%; Pred. No. 5.9e-26;
 Matches 84; Conservative 63; Mismatches 144; Indels 7; Gaps 5;

QY 16 DYAAAFNCCTDENI-PLKMHYLPVIGIIFLVGFGNAVITYITFKMRPKMSSTIMLN 74
 Db 21 DYEGAL-PCERSNVKELAAQFLPLYSLVEMIGLVVVVVVILTKRKRLRMNTNYL 79
 QY 75 LACTDILYLTSLPELIHYVAGSEWIGDPMCKFRIRSFHFNYSILFLCPSIFRYCV 134
 Db 80 LAISDVLEFVTLPLPWH-YRKRMKMGCHMKLSLYMGIXSELIFFIITLIDYXIA 138
 QY 135 ITHMCSFSIHKTCAVAVACAVVITISLVAVIEMTFLITSTNRTNSACIDLASSDELNT 194
 Db 139 IVHAVFLRARTVTFGLVTSIFTWGLAGLALPEFFHEHFOEAGLTICSPYLPENNVNA 198
 QY 195 IKWYN-LITATFCLPIVITVLCYTIITHTLHGLOTDSLOKARRLTILLAAVYVC 253
 Db 199 WKQPHALRMNIGLALPLVAVACYSGIITLT--LCPKSKTKAIRLIFVIMVVFIF 255
 QY 254 FLPEHILVIRIESRLISCSISLQSIENQTHEAYIVSRPLAANTFGLLLYVVSNDPQO 311
 Db 256 WTPFNLVLVLLAFQMHLETCDEOSROLDLMLVTEVIALYHCCNPNYIAVFGERRFK 313

RESULT 14
 Q9MZM1 PRELIMINARY; PRT; 347 AA.

AC Q9MZM1;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Chemokine receptor CXCR4 (Fragment).
 GN CXCR4.
 OS Eulemur macaco (Pteropus macaco).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.
 RX NCBI_TaxID=30602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
 Primates.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF172242; AAF89362.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR000306; Ig_MHC.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR01558; CHEMOKINER1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR01568; LYMPHOTACTIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; 1.

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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:36:28 ; Search time 22 Seconds

(without alignments)
635.342 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVSGNLEPAKKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	32.5	373	1 P2YR_MOUSE	P49650 mus musculu
2	567	32.0	373	1 P2YR_HUMAN	P47900 homo sapien
3	565.5	31.9	362	1 P2YR_CHICK	P49652 gallus gall
4	565.5	31.9	362	1 P2YR_MEIGA	P49651 rattus norv
5	565	31.9	373	1 P2YR_RAT	P48042 bos taurus
6	562	31.7	373	1 P2YR_BOVIN	P79928 xenopus lae
7	557	31.5	337	1 P2YR_XENLA	P51582 homo sapien
8	514	29.0	361	1 P2Y4_HUMAN	O35811 rattus norv
9	512	28.9	361	1 P2Y4_RAT	O91347 mus musculu
10	503	28.4	361	1 P2Y4_MOUSE	O98907 gallus gall
11	492	27.8	368	1 P2Y3_CHICK	O98975 homo sapien
12	487.5	27.5	346	1 CLT2_HUMAN	O93361 meleagris g
13	486.5	27.3	328	1 P2Y3_MEIGA	P41232 rattus norv
14	483.5	27.0	374	1 P2Y2_RAT	P41231 mus musculu
15	479	26.8	373	1 P2Y2_MOUSE	O95n03 sus scrofa
16	474	26.0	377	1 P2Y2_HUMAN	O92081 mus musculu
17	452	25.5	345	1 CLT2_PIG	O92081 mus musculu
18	442.5	25.0	309	1 CLT2_MOUSE	O92081 mus musculu
19	430	24.3	309	1 CLT2_RAT	O92081 mus musculu
20	423	23.7	328	1 P2Y6_RAT	O63371 rattus norv
21	419.5	23.7	420	1 PARI_XENLA	P67749 xenopus lae
22	405	22.9	328	1 P2Y6_HUMAN	O15077 homo sapien
23	404	22.8	430	1 PARI_MOUSE	P30508 mus musculu
24	397	22.4	357	1 CKR9_HUMAN	P31666 homo sapien
25	396.5	22.4	432	1 PARI_RAT	P26874 rattus norv
26	395.5	22.3	367	1 CKR9_MOUSE	O9wut7 mus musculu
27	394.5	22.3	367	1 GP17_HUMAN	O13304 homo sapien
28	391	22.1	428	1 PARI_CRITIO	O00991 cricetus
29	389.5	22.0	425	1 PARI_PAPHA	P56488 papio hamad
30	388.5	21.9	399	1 PARI_MOUSE	P35086 mus musculu
31	386.5	21.8	425	1 PARI_HUMAN	P56488 mus musculu
32	383.5	21.7	397	1 PARI_RAT	O63645 rattus norv
33	380	21.5	308	1 P2Y5_CHICK	P32250 gallus gall

ALIGNMENTS

RESULT 1	ID	P2YR_MOUSE	STANDARD	PRT	373 AA
AC	P49650:				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).				
GN	P2Y1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Insulinoma;				
RA	MEDLINE=95298025; PubMed=7779087;				
RT	Yokoyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;				
RL	"Cloning of rat and mouse p2y purinoceptors."				
RL	Biochem. Biophys. Res. Commun. 211:211-218(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/Sv;				
RA	Leon C.;				
RT	"Thromboresistance in p2y1 receptor knockout mice."				
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS				
CC	ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS				
CC	OF EXTRACELLULAR ATP ON INSULIN SECRETION.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	-----				
DR	EMBL; U22829; AAA91302.1; -				
DR	EMBL; AJ245636; CAB57317.1; -				
DR	HSSP; P34996; 1DD.				
DR	MGI; MGI:105049; P2Y1.				
DR	InterPro: IPR000276; GPCR_Rhodopsin.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PRINTS; PR00237; GPCRHOOPS.				
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.				
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1 52				
FT	TRANSNEM 53 74				
FT	DOMAIN 75 87				
FT	TRANSNEM 88 109				
FT	DOMAIN 110 126				
FT	TRANSNEM 127 147				
FT	TRANSNEM 127 147				


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FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 308 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 309 329 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42212 MW; 944125E9F4560B3 CRC64;

Query March 32.5%; Score 575; DB 1; Length 373;
Best Local Similarity 36.5%; Pred. No. 6.3e-31;
Matches 109; Conservative 67; Mismatches 119; Indels 4; Gaps 2;

QY 24 CTDENIPDKMAYLVIVGIIFLNGCPGNAVIVSYIFKMRPMKSTIIMLNACTDLIYL 83
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 42 CALKRTGQFQYVLPVAVIIVFIIIFLGNSVAIMFVFMKRWGSLVYMFLALADFLYV 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 84 TSLPPLHYVAGSNWIFGDMCKFIRSFHFNLVYSSILFLTFCISFRVYVLIHPMCSFS 143
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 102 LTFLLALFFYFNKTDWIFGDMCKKRFIFHVNLYGSLFLTFCISAHRYSGVYVPLKSLG 161
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 IHRRCVAVACAVVMIISLVAVIMPTFLITSTNPNRS-ACGLDSSDELMTIKYNIL 202
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 162 RLKKNALVSVLVVAVIIVAVISPLFSGTGTRKNKVTQVDTSSNDLSYFLYSMCT 221
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 TATFCEPLVIVLYVLTITHTLHGLQTDSCOKANRLTLLLAFFVCFELPFIILRV 262
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 222 TVAFCEIPVLVILICGYGLIVAKALYNDLNSPLRKRKSYIVIVYVAVSYIFPHWKT 281
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 IRISRL---LSISCSIEHQHEAVYISRPALANTGNLLIYVVSNDFOAVCSIVR 318
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 282 MNLARLDFQTPENCDFNDRYATYATYVGRGLASNCVDPILYFLAGDTFRRRLSRATR 340
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
P2YR_HUMAN STANDARD; PRT; 373 AA.
ID P2YR_HUMAN STANDARD; PRT; 373 AA.
AC P47900;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta; PubMed=8666290;
RX MEDLINE=96257237; PubMed=8666290;
RA Leon C., Vial C., Cazenave J.-P., Gachet C.;
RT "Cloning and sequencing of a human cDNA encoding endothelial P2Y1
RT purinoceptor."
RL Biochem. Biophys. Res. Commun. 218:783-788(1996).
RP SEQUENCE FROM N.A.
RX MEDLINE=96205320; PubMed=8630005;

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RA Janssens R., Commun D., Piroton S., Samson M., Parmentier M.,
RA Boeynaems J.M.;
RT "Cloning and tissue distribution of the human P2Y1 receptor.";
RL Biochem. Biophys. Res. Commun. 221:588-593(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Leon C., Vial C., Weber J., Cazenave J.-P., Gachet C.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES.
RC TISSUE=Platelet;
RX MEDLINE=98113162; PubMed=9442040;
RA Jin J., Daniel J.L., Kunapuli S.P.;
RT "Molecular basis for ADP-induced platelet activation. II. The P2Y1
RT receptor mediates ADP-induced intracellular calcium mobilization and
RT shape change in platelets.";
RL J. Biol. Chem. 273:2030-2034(1998).
CC -I- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP. IN PLATELETS BINDING TO ADP LEADS TO MOBILIZATION OF
CC INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C, A
CC CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET AGGREGATION.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- INDUCTION: REPRRESSED BY THE P2Y1 RECEPTOR-SPECIFIC ANTAGONISTS
CC A2P5P, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION MOBILIZATION
CC AND SHAPE CHANGE IN PLATELETS.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; Z49205; CAA89066.1; -
DR EMBL; U42030; AAA97873.1; -
DR EMBL; U42029; AAA97872.1; -
DR EMBL; S81950; AAB47091.1; -
DR EMBL; AJ006945; CAA07339.1; -
DR EMBL; AF018284; AAB94556.1; -
DR HSSP; P34996; 1DDO.
DR Genew; HGNC:8539; P2RY1.
DR MIM; 601167; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECPR_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECPR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
KW Blood coagulation.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 308 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 309 329 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 138 138 MISSING (IN REF. 1).

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Seq	Sequence	373 AA	42071 MW	4DC7C668BB4145392 CRC64
Q0	SEQUENCE	373 AA	42071 MW	4DC7C668BB4145392 CRC64
Q1	Query Match	32.0%	Score 567	DB 1; Length 373
Q2	Best Local Similarity	36.1%	Pred. No. 2.1e-30	
Q3	Matches 108; Conservative	68; Mismatches 119; Indels	4; Gaps	2;
Q4	CTDENIPFLKMHVLPVIGIIFVGFPEGNNAVVISIRFKMRPMKSTIIMNLACTDILYL	83		
Q5	42 CALRTGFGFQRYLPVAVILVFIIGFGLNSVAIMFVHMKWSGISVYMENLALADLXY	101		
Q6	84 TSLPELHYVAGSGENMIFGDMCFKIFRPFHNLVYSLIFLTCESIRFYCIHHPMCS	143		
Q7	102 LTPALPIFYFNKTDWIFGDMCKLQRFHFVNLKSLIFLTCISAHRSYVVPPLNSLG	161		
Q8	144 IHTRCVAVCAVAVMIISLVAVIPMFLITSTNFTNS-ACLDLTSSDELNTIKWNLIL	202		
Q9	162 RLKKNKACISGLVWMLVVAISPILFYSGVGVRKNTICYDTPSDSEYLRSPYISMC	221		
Q10	203 TATTFCLPVIYVILCTYTIITLHTLHGQDTSCLOKAKRRLTILLALFYVCLPFIHIV	262		
Q11	222 TVAFECVPLVILIGCYGLVYALYKLDNSPLRKRSIYVILVTFVAFVYIPFHWT	281		
Q12	263 IIRISRI---LSISCSIEINOHEAVYISRPALNTFGNLLLVVSNFOAVCSYVR	318		
Q13	282 MNLKARLDFOTPMACAFENDRYATVYVTRGLASLNSCVDPILTYLAGDTEFRRLSRATR	340		
Q14	RESULT 3			
Q15	P2YR_CHICK			
Q16	ID P2YR_CHICK	STANDARD;	PRF;	362 AA.
Q17	AC P34996;			
Q18	DT 01-FEB-1994 (Rel. 28, Created)			
Q19	DT 01-FEB-1994 (Rel. 28, Last sequence update)			
Q20	DT 15-DEC-1998 (Rel. 37, Last annotation update)			
Q21	DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).			
Q22	GN P2Y1.			
Q23	OS Gallus gallus (Chicken).			
Q24	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Q25	OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
Q26	OC Gallus.			
Q27	OX NCBI_TaxID=9031;			
Q28	RN [1]			
Q29	RN SEQUENCE FROM N.A.			
Q30	RP TISSUE=Brain;			
Q31	RC MEDLINE=93285340; PubMed=8508924;			
Q32	RA Webb T.E., Simon J., Krishnek B.J., Bateson A.N., Smart T.G.,			
Q33	RA King B.F., Burnstock G., Barnard E.A.;			
Q34	RT "Cloning and functional expression of a brain G-protein-coupled ATP			
Q35	RT receptor.";			
Q36	RL FEBS Lett. 324:219-225(1993).			
Q37	RL [2]			
Q38	RP 3D-STRUCTURE MODELING.			
Q39	RX MEDLINE=97026278; PubMed=8872457;			
Q40	RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;			
Q41	RL "Modelling the P2Y purinoceptor using rhodopsin as template.";			
Q42	RL Drug Des. Discov. 13:133-140(1995).			
Q43	CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS			
Q44	CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN			
Q45	CC INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT			
Q46	CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
Q47	CC -1- SUBCELLULAR LOCATION: Integral membrane protein.			
Q48	CC -1- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT,			
Q49	CC SPLEEN AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,			
Q50	CC STOMACH, LUNG AND KIDNEY.			
Q51	CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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Q57	CC entities requires a license agreement (see http://www.isb-sib.ch/announce/			
Q58	CC or send an email to license@isb-sib.ch).			

[illegible]

OC Archosauria: Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 ON NCBI_TaxID=9103;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=94335907; PubMed=8058061;
 RA Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
 RT "Expression of a cloned p2y purinergic receptor that couples to
 RL phospholipase C.";
 RN Mol. Pharmacol. 46:8-14(1994).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97382456; PubMed=9240460;
 RA Li Q., Schachter J.B., Harden T.K., Nicholas R.A.;
 RT "The 6H1 orphan receptor, claimed to be the p2y5 receptor, does not
 RT mediate nucleotide-promoted second messenger responses.";
 RL Biochem. Biophys. Res. Commun. 236:455-460(1997).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
 CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
 CC INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: MAINLY FOUND IN BLOOD, BRAIN, AND LUNG. TO A
 CC LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: U09842; AAA18784.1; -
 DR EMBL: AF012103; AAB65428.1; -
 DR HSSP: P34996; 1DDP.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1.1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1.2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 41
 FT TRANSMEM 42 63
 FT DOMAIN 64 76
 FT TRANSMEM 77 98
 FT DOMAIN 99 115
 FT TRANSMEM 116 136
 FT DOMAIN 137 155
 FT TRANSMEM 156 177
 FT DOMAIN 178 207
 FT TRANSMEM 208 227
 FT DOMAIN 228 254
 FT TRANSMEM 255 274
 FT DOMAIN 275 292
 FT TRANSMEM 293 317
 FT DOMAIN 318 362
 FT DISULFID 113 191
 FT CARBOHYD 11 11
 FT CARBOHYD 26 26
 FT CARBOHYD 102 102
 FT CARBOHYD 186 186
 SQ SEQUENCE 362 AA; 41180 MW; 3E128AB9EB64349C CRC64;
 Query Match 31.98; Score 565.5; DR 1; Length 362;
 Best Local Similarity 35.08; Pred. No. 2,5e307;
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

QY 54 VISTYFKRMPKWSSTITMLNACTDLTYLTSPLFLHYHVAAGENMIFGPKCFIRESE 113
 Db 61 AWMFVFMHBMWGSISYFMENLADFLVTLTALIFYYFNKDTFGDVCKLGRFIF 120
 QY 114 HFNYSSTLFTGCSIFRCVVIHHPMCSFSEIHKTRCVAVACAVWIISLVAVIMPLLI 172
 Db 121 HVDLYGSILFLTCISVHRYGVVHPKSLGRLKKNVYSSLVWALVAVIATLFTYSG 180
 QY 173 TSTNRTSRASCLDTSSDEINIKWVILITATTCFLPVLVLCYTIITHTLHGLQTD 232
 Db 181 TGVRRNKTTTCYPTTADENYRSFYVSMCTVMEFCIFVILIGCYGLYKALIKOLDN 240
 QY 233 SCLKQKARLTILLALAFYCELPFHILVIRIESRL---LSISCSITENDIHEATYVSR 289
 Db 241 SPLRRKSIYVITVLTFAVSYLPFHVKMTLNRARLDFOTPOMCAFNDKRYATYQVTRG 300
 QY 290 LALNFRGNLLIVVYSDNFOQVCSVR 318
 Db 301 LASLNSCVDPILFTYAGDTFRRLSRATR 329
 RESULT 5
 ID P2YR_RAT STANDARD; PRT; 373 AA.
 AC P49651;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 01-FEB-1996 (Rel. 33, Last annotation update)
 GN P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Insulinoma;
 RA MEDLINE=95298025; PubMed=7779087;
 RX Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
 RT "Cloning of rat and mouse p2y purinoceptors.";
 RL Biochem. Biophys. Res. Commun. 211:211-218(1995).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
 CC ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS
 CC OF EXTRACELLULAR ATP ON INSULIN SECRETION.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,
 CC LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: U22830; AAA91303.1; -
 DR HSSP: P34996; 1DDP.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1.1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECP_F1.2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 52
 FT TRANSMEM 53 74
 FT DOMAIN 75 87
 FT TRANSMEM 88 109
 FT DOMAIN 110 126
 FT TRANSMEM 127 147
 FT DOMAIN 148 166
 FT TRANSMEM 167 188
 SQ SEQUENCE 188 AA; 21180 MW; 3E128AB9EB64349C CRC64;

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FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 42321 MM; 6DDF676287B5E648 CRC64;
SQ SEQUENCE 373 AA;

Query Match 31.9%; Score 565; DB 1; Length 373;
Best Local Similarity 36.1%; Pred. No. 2.8e-30;
Matches 107; Conservative 67; Mismatches 113; Indels 4; Gaps 2;

QY 32 KMHLPIYGIIFLPGFPGNAVISTYIFKMRPKSSTIIMLNACTDLYLSPLFIH 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 50 QFYLPVAVILVFIIFLGNSVAIMFVHKPKSGISVYFMNLADFLVLPALIF 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 92 YVASEGNIIFGDECKFIRESFHNLYSILFLCFISFYCVIHPMSGCSHKTRCAV 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 110 YFVKTDWIFGDMCKLQRFIFHNLYGSLFLCISAHRSYGVPYPLKSLGRKKNAI 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 152 VACAVVWILSVAVIPMTFLTSNTRNRS-ACLDLTSDELNTIKYNLLTFTCLP 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 170 YVSVLWLVVAVLVAISPFIETSGTIRKKNVTCYDSDELSRSTFYISMTYVAMEFIP 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 211 LVIVTLGYTIIHTLFGLOTDSCLKOKARRLTILLAFYCEPFIHLVIRIESRL- 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 230 LVLLIGCGGLVRLVLYIKDLNLSRLKRSIYLVIVLVFAVSIPIFPVMTMNLRALD 289
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 270 --LSISCSIEQIHEAVYSRPLAALNTEGULLYVVVSNFQOAVCSTVR 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 290 FQPEMCDPNDRVATYATQVTRGLASLNSCVDPIILYFLAGDTFRRLSRATR 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
P2YR_BOVIN STANDARD; PRT; 373 AA.
AC P48042;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus callosum;
RX MEDLINE=99064562; PubMed=9848096;
RA Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;
RT "Cloning and expression of a P2Y purinoceptor from the adult bovine
RL corpus callosum."
RL Neurobiol. Dis. 5:259-270(1998).
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----

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CC -----
DR EMBL; X87628; CA60958.1; -
DR EMBL; U34041; AAC78275.1; -
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 87 2 (POTENTIAL).
FT TRANSMEM 88 109 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 110 126 3 (POTENTIAL).
FT TRANSMEM 127 147 4 (POTENTIAL).
FT TRANSMEM 148 166 5 (POTENTIAL).
FT TRANSMEM 167 188 6 (POTENTIAL).
FT TRANSMEM 189 218 7 (POTENTIAL).
FT TRANSMEM 219 238 8 (POTENTIAL).
FT TRANSMEM 239 265 9 (POTENTIAL).
FT TRANSMEM 266 285 10 (POTENTIAL).
FT TRANSMEM 286 303 11 (POTENTIAL).
FT TRANSMEM 304 328 12 (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 42287 MM; 9270A7175C0BDA76 CRC64;
SQ SEQUENCE 373 AA;

Query Match 31.7%; Score 562; DB 1; Length 373;
Best Local Similarity 36.1%; Pred. No. 4.4e-30;
Matches 108; Conservative 67; Mismatches 120; Indels 4; Gaps 2;

QY 24 CTDENIPLKMHVLPVYGIIFLPGFPGNAVISTYIFKMRPKSSTIIMLNACTDLYL 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 42 CALRTKGQFYLPVAVILVFIIFLGNSVAIMFVHKPKSGISVYFMNLADFLYV 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 84 TSLPFLHYVASEGNIIFGDECKFIRESFHNLYSILFLCFISFYCVIHPMSGCS 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 102 LTLPALIYVFNKTDWIFGDMCKLQRFIFHNLYGSLFLCISAHRSYGVPYPLKSLG 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 IHKTRCAVACAVVWILSVAVIPMTFLTSNTRNRS-ACLDLTSDELNTIKYNLL 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 162 RLKKNNAVYISVLWLVVAVISPFIETSGTIRKKNVTCYDSDELSRSTFYISMT 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 TATFPCPLVIVTLCYTTIHTLFGLOTDSCLKOKARRLTILLAFYCEPFIHLVIR 262
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 222 TVAMFCVPLVILGCGYLVRLVLYIKDLNLSRLKRSIYLVIVLVFAVSIPIFPV 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 IRISSRL--LSISCSIEQIHEAVYSRPLAALNTEGULLYVVVSNFQOAVCSTVR 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 282 MNLRARLDFQPEMCAFNDRVATYATQVTRGLASLNSCVDPIILYFLAGDTFRRL 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
P2Y8_XENLA STANDARD; PRT; 537 AA.
AC P79928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE P2Y purinoceptor 8 (P2Y8).
GN P2RY8.

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OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neural plate;
 RA MEDLINE=97284734; PubMed=9139711;
 RX Bogdanov Y.D., Dale L., King B.F., Whitlock N., Burnstock G.;
 RT "Early expression of a novel nucleotide receptor in the neural plate
 of Xenopus embryos.";
 RL J. Biol. Chem. 272:12583-12590(1997).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP, UTP, GTP AND TTP.
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: X99593; CAA68213.1; -
 DR HSSP: P34996; IDDD
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49
 FT TRANSSEM 50 70
 FT TRANSSEM 71 79
 FT TRANSSEM 80 100
 FT TRANSSEM 101 118
 FT TRANSSEM 119 139
 FT TRANSSEM 140 161
 FT TRANSSEM 162 182
 FT TRANSSEM 183 210
 FT TRANSSEM 211 231
 FT TRANSSEM 232 254
 FT TRANSSEM 255 275
 FT DOMAIN 276 292
 FT TRANSSEM 293 316
 FT DOMAIN 317 537
 FT DISULFID 116 193
 FT CARBOHYD 26 29
 FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 537 AA; 62024 MW; B2CF24812F3C19E2 CMC64;
 Query Match 31.5%; Score 557; DB 1; Length 537;
 Best Local Similarity 34.2%; Pred. No. 1.3e-29;
 Matches 116; Conservative 70; Mismatches 139; Indels 14; Gaps 4;

DB 194 HDTTRPEDFARVVESTAIKMLFCIGPOLIAGCGIMTRRLMPYVSGNOOTLPSYKRR 253
 QY 239 ARRLTIILLFLAFYOCFPHILRYIRISRLISTSCSLENOIHEAYTSPRLALNTEGN 298
 DB 254 SIKTIIFWIAFCEMPEHTRITRYRYARLLGICVLANVNTYKTVRLPLASNSCID 313
 QY 299 LLLVYVSDNFQAVCSYRCKVSGNLEQAKRISYNNP 337
 DB 314 PLYFLANDRRRLRIIRVRRRSS---VPNRCHMTNRP 349
 RESULT 8
 P2Y4_HUMAN
 ID P2Y4_HUMAN STANDARD: PRT; 365 AA.
 AC P51582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P).
 GN P2RY4 OR NRU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96125055; PubMed=8537336;
 RA Communi D., Piroton S., Parmentier M., Boeynaems J.-M.;
 RT "Cloning and functional expression of a human uridine nucleotide
 RT receptor.";
 RL J. Biol. Chem. 270:30849-30852(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96125054; PubMed=8537335;
 RA Nguyen T., Erb L., Weisman G.A., Marchese A., Heng H.H.Q.,
 RA Garrard R.C., George S.R., Turner J.T., O'Dowd B.F.;
 RT "Cloning, expression, and chromosomal localization of the human
 RT uridine nucleotide receptor gene.";
 RL J. Biol. Chem. 270:30845-30848(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=96197801; PubMed=8617367;
 RA Stam N.J., Klopff J., van der Heuvel M., Olijve M.;
 RT "Molecular cloning and characterization of a novel orphan receptor
 RT (p2p) expressed in human pancreas that shows high structural homology
 RT to the p2U purinoceptor.";
 RL FEBS Lett. 384:260-264(1996).
 CC -1- FUNCTION: Receptor for UTP and UDP coupled to G-proteins that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC NOT activated by ATP or ADP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Pancreas.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: X91852; CAA62963.1; -
 DR EMBL: U40223; AAC50347.1; -
 DR EMBL: X96597; CAA65415.1; -
 DR HSSP: P34996; IDDD.
 DR Genew: HGNC:8542; P2RY4.
 DR MIM: 300038; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: P500237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: P50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Polymorphism.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 35 61 1 (POTENTIAL).
 FT DOMAIN 62 72 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 73 95 2 (POTENTIAL).
 FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 113 131 3 (POTENTIAL).
 FT DOMAIN 132 154 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 155 174 4 (POTENTIAL).
 FT DOMAIN 175 196 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 197 222 5 (POTENTIAL).
 FT DOMAIN 223 246 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 247 269 6 (POTENTIAL).
 FT DOMAIN 270 287 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 288 309 7 (POTENTIAL).
 FT DOMAIN 310 365 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 108 185 BY SIMILARITY.
 FT VARIANT 168 188 V -> M (IN DBSNP:1152186).
 FT VARIANT 178 188 N -> T (IN DBSNP:1152187).
 FT VARIANT 191 191 P -> L (IN DBSNP:1152188).
 FT VARIANT 191 191 P -> L (IN DBSNP:1152188).
 FT CONFLICT 86 86 L -> V (IN REF. 2).
 FT CONFLICT 234 234 S -> A (IN REF. 2).
 SQ SEQUENCE 365 AA; 40963 MW; 23E0AFED3B7BDEED CRC64;

Query Match 29.0%; Score 514; DB 1; Length 365;
 Best Local Similarity 35.1%; Pred. No. 5.7e-27;
 Matches 101; Conservative 64; Mismatches 119; Indels 4; Gaps 2;

QY 26 DENILKMHVPIVIGIIFLPGFNNAVISTYIFKMRPMKSTIIMNLACTDILYLS 85
 DB 30 DED--FKTILPVSIAVAVFVLGLNAPLTLFIRLRWDATFATYMEFLASDLYLVS 87
 QY 86 LPFLHYASGEMWIFGDMCKFRFSEFHNLYSILFLTCISIFRCYIIHMSQFSIH 145
 DB 88 LPTLYYYAAHNMHFGTEICKFVFLFWMNYCGLVPLTCTSVHRIGICHPRLRLMG 147
 QY 146 KTRCAVACAVVWIIISLVAVVPMLITSTNRTNSACIDLTSSDELNTIKYNNILAT 205
 DB 148 RPLRLAGLCLAVLWVAGCLVPLNLFVVTSSNGTIVLCHDTRPEEFDHVHSSAVML 207
 QY 206 TFCLELVYITLCYTTIITHTLHGL--QIDSCAKQARRTITILLAFYCFPLHLYI 263
 DB 208 LFGVCLVTVLCYGLMARLXPLPGSAGSSSRSLRLTIAVLLVYFAVCFVPHITRTI 267
 QY 264 RIESRLSISCSIEHQIHEAVYIVSRPLALNTFGNLLVYVSDNQ 311
 DB 268 YLALRLLEADRCVNLINVVNYKTRPLASNSCLDPVLYLLGDKYR 315
 RESULT 9
 P2Y4_RAT
 ID P2Y4_RAT STANDARD: PRT; 361 AA.
 AC 035811:
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 4 (P2Y4).
 GN P2Y4 OR P2Y4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RA Bogdanov Y.D., Wildman S., King B.F., Burntack G.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98421785; PubMed=9751165;
 RA Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
 RL "Molecular cloning and characterization of the rat P2Y4 receptor."
 J. Neurochem. 71:1424-1434(1998).
 CC -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 activate a phosphatidylinositol-calcium second messenger system.
 CC Not activated by ADP or UDP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,
 CC higher expression in the pineal gland and ventricular system.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: Y14705; CAA75007.1; -
 DR EMBL: Y14433; CAA72241.1; -
 DR HSSP: P34996; 1DDO.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PR00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: P500237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: P50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 69 91 2 (POTENTIAL).
 FT DOMAIN 92 108 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 109 127 3 (POTENTIAL).
 FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 150 170 4 (POTENTIAL).
 FT DOMAIN 171 192 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 193 218 5 (POTENTIAL).
 FT DOMAIN 219 242 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 243 265 6 (POTENTIAL).
 FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 284 305 7 (POTENTIAL).
 FT DOMAIN 306 361 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 104 181 BY SIMILARITY.
 FT CARDHYD 175 175 N-LINKED (GLCNAC.) (POTENTIAL).
 SQ SEQUENCE 361 AA; 40893 MW; 0377F96E54B449A3 CRC64;
 Query Match 28.9%; Score 512; DB 1; Length 361;
 Best Local Similarity 34.2%; Pred. No. 7.6e-27;
 Matches 105; Conservative 66; Mismatches 126; Indels 10; Gaps 4;
 QY 15 PDYAAFGNCIDENIPDKMHVPIVIGIIFLPGFNNAVISTYIFKMRPMKSTIIMNL 74
 DB 14 PSPSGDGDGR--FNEEFKTIILPMGAVAVFVLGLNAPLTLFIRLRPMATATYMH 72
 QY 75 IACTDLVYTSPLFLHYASGEMWIFGDMCKFRFSEFHNLYSILFLTCISIFRCV 134
 DB 73 LALSDTLVYLSPTLYYYAAHNMHFGTEICKFVFLFWMNYCGLVPLTCTSVHRIG 132
 QY 135 ITHPMSCFSIHKTRCAVACAVVWIIISLVAVVPMLITSTNRTNSACIDLTSSDELNT 194
 DB 133 ICHPLRAIRWGRPRASLILCLGFWLVVAGCLVPLNLFVVTSSNGTIVLCHDTPLEEDH 192
 QY 195 IKWNYLITATFCPLVITLCYTTIITHTLHGL----QIDSCAKQARRTITILLAF 250
 DB 193 YTFSSAVAVLLFGLPELITLVLCYGLMARLXPLPGAGQSSRL--SLRTIAYVLYV 250
 QY 251 YVCELPFHILRYIRIESRLSISCSIEHQIHEAVYIVSRPLALNTFGNLLVYVSDNQ 310
 DB 251 AVCFVPHITRTIYVQARLLQADCVNLINVVNYKTRPLASNSCLDPVLYLLGDKYR 310


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QY      311 ---QAVC 314
Db      311 NQLOQLC 317

RESULT 10
P2Y4_MOUSE
ID      P2Y4_MOUSE      STANDARD;      PRT;      361 AA.
AC      09JUS7;
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DE      P2Y purinoceptor 4 (P2Y4).
GN      P2RY4 OR P2Y4R.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SVJ;
RX      MEDLINE=21185993; PubMed=11290369;
RA      Suarez-Huerta N., Pouillon V., Boeynaems J.-M., Robaye B.;
RT      "Molecular cloning and characterization of the mouse P2Y4 nucleotide
      receptor."
RL      Eur. J. Pharmacol. 416:197-202(2001).
CC      -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
      activate a phosphatidylinositol-calcium second messenger system.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: Expressed in the liver, intestine, stomach,
      bladder and lung.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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      entities requires a license agreement (See http://www.isb-sib.ch/announce/
      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, AJ277752; CAB91043.1; -.
DR      HSSP; P34996; IDDD.
DR      MGD; MGI:1926594; P2Y4.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm.1; 1.
DR      PRINTS; PR00237; GPCRHOOPS.
DR      PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; 1.
DR      PROSITE; PS50262; G-PROTEIN_RECPT_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
FT      DOMAIN 1 31 58
FT      TRANSSEM 59 68
FT      TRANSSEM 69 91
FT      TRANSSEM 92 108
FT      TRANSSEM 109 127
FT      TRANSSEM 128 149
FT      TRANSSEM 150 170
FT      TRANSSEM 171 192
FT      TRANSSEM 193 218
FT      TRANSSEM 219 242
FT      TRANSSEM 243 265
FT      TRANSSEM 266 283
FT      TRANSSEM 284 305
FT      TRANSSEM 306 361
FT      DOMAIN 104 181
FT      DISULFID 175 175
FT      CARBOHYD 41034 MW; 3E8EA84B5BC0A20 CRC64;
SQ      SEQUENCE 361 AA; 41034 MW; 3E8EA84B5BC0A20 CRC64;

Query Match      28.4% Score 503; DB 1; Length 361;
Best Local Similarity 33.9%; Pred. No. 2.9e-26;
Matches 107; Conservative 65; Mismatches 134; Indels 10; Gaps 4;

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QY      6 DYLANASDPDYAAAFNGCTDENIPKMHLPVYIGLIFVFGPNNAVSTYIFKMPW 65
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      5 DSLFTSLGSPSSGDDGC-KFNEEFKTLPLSAVAVFGLALNAPTLWLFRLRPW 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      66 KSTTIMINLACTDLVLTSPFLIHYASGNNIFGDMCKTFRSFHFLYSSILFLT 125
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 DATATYMEHLALSTLYLVLSPLTVVYVYAAHNHMFPGFGCKFVRFLEYNNLYCSVLELT 123
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      126 CFSIFRCVLIHPMSGCSIHTRCAVAVACVAVVILSLAVIPMFELTSTRTKRSACLD 185
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      124 CTSVHRWIGICHPLAIRMWRPRRAGLCLGVLVAGCLVPLNFFVTTNANGTTIICHD 183
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      186 LTSSDELNTIKMYMLILATFCLPLVIVLYCYTTIIHTLTHGL----QEDSCRKORAR 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      184 TLPEEPDHYVYFSTTIVLLFGPPLITIVCYGLMARRLYRPLPGAGQSSRL- RSLR 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      242 LTIILLAFVYCLPFIHLRYIRIESRLISCSIEQIHFAIYVSRIALALNFGNILL 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      242 TIAVLVAVFVAVCFPFHTRITRYIARILNAECHEVLNIVNVVYKTRPLASANCLDPVL 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      302 YVVVSDNFO--QAVC 314
Db      302 YLFTGDKYRNQQLC 317

RESULT 11
P2Y3_CHICK
ID      P2Y3_CHICK      STANDARD;      PRT;      328 AA.
AC      098907;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      16-OCt-2001 (Rel. 40, Last annotation update)
DE      P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN      P2RY3.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=96319774; PubMed=8700132;
RA      Webb T.E., Henderson D., King B.F., Wang S., Simon J.,
RT      Bateson A.N., Burnstock G., Barnard E.A.;
RT      "A novel G protein-coupled P2 purinoceptor (P2Y3) activated
      preferentially by nucleoside diphosphates."
RL      Mol. Pharmacol. 50:258-265(1996).
CC      -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADP > UTP > ATP - UDP. THE
      ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
      A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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      entities requires a license agreement (See http://www.isb-sib.ch/announce/
      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X98283; CAAB6930.1; -.
DR      HSSP; P34996; IDDD.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm.1; 1.
DR      PRINTS; PR00237; GPCRHOOPS.
DR      PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; FALSE_NEG.
DR      PROSITE; PS50262; G-PROTEIN_RECPT_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
FT      DOMAIN 1 23 43
FT      TRANSSEM 23 43
FT      TRANSSEM 43 63

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FT DOMAIN 44 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 2 (POTENTIAL).
FT DOMAIN 79 96 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 97 117 3 (POTENTIAL).
FT DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 160 4 (POTENTIAL).
FT DOMAIN 161 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 210 5 (POTENTIAL).
FT DOMAIN 211 231 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 252 6 (POTENTIAL).
FT DOMAIN 253 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 298 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 299 323 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SULFID 94 172 BY SIMILARITY.
SQ SEQUENCE 328 AA; 37586 MW; 7A3BF1C91F54FAB CRC64;

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Query Match 27.88; Score 492; DB 1; Length 328;
Best Local Similarity 35.28; Pred. No. 1.4e-25;
Matches 117; Conservative 56; Mismatches 139; Indels 20; Gaps 9;

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QY 16 DVAARNGCTDENIPKMHVPIYGIIFLPGPGNAVISTYIFKMRPKSSTIMLN 75
DB 5 NFGGRNSCFEHE-EKQVLLPLVSVFLLGLPLNAVIGQIMLRKALTFTTYMLN 63
QY 76 ACTDLITLPLIHYVAGSENMIFGDFCKFRSFHNLXSILFLTCFIFRCV 135
DB 64 AMADLLYCSLPILITNYOKOVWPGDFCKFRVROFYNHLSILFLTCISVORMG 123
QY 136 IHMPCFSJHK--TRCAVAVACAVWIIISLAVIIMPFLITST-NRTNSACLDLTSSDE 191
DB 124 CHELA--SWHKKKGKGLTWLVCNAVWFIYAQCLP-TFEVASTGTORNRTVCYDLSPPDR 180
QY 192 LMTIKYNNLLATFTCLPLVLYTLCYTIHHTLHGLQDLSL-----KKARLRTI 244
DB 181 STSYEPYGITLTITGLLPPAALACYSMARLL---CKDELIGLAVHKKKRAVAMIT 237
QY 245 LLLAFYVCFPLPHIRVIRIESR-LLSISCSIEQIHEAYISRLPAATFNGLLLYV 303
DB 238 IYIVYSISFPFHLKITYLYRSASLPCPLQAFAIAKYKTRFPASNSVLDPLIF 297
QY 304 VSDNFQAVCVSTVRCKVSGNLEQAKISYSN 335
DB 298 FTQRKPREST-RYLLDKMSSKWRQDHCISYGS 328

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RESULT 12.
CUT2_HUMAN STANDARD; PRT; 346 AA.
ID AC Q9NS75; Q9HCQ2;
AC 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321).
GN CysLTR2 OR CysLTR2 OR CysLTR2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20374466; PubMed=10913337;
RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
RA Nishikawa T., Kawai Y., Masuno Y., Isogai T., Suzuki Y., Sugano S.,
RA Furuichi K.;
RT "The molecular characterization and tissue distribution of the human
RL cysLT2 leukotriene receptor.";
RL Biochem. Biophys. Res. Commun. 274:316-322(2000).
RP SEQUENCE FROM N.A.
RX MEDLINE=20459128; PubMed=10851239;
RA Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,

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RA Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
RA Williams D.L. Jr., Zeng Z., Liu O., Ma L., Clements M.K., Coulombe N.,
RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
RA Lynch K.R., Evans J.F.;
RT "Characterization of the human cysLT2 leukotriene 2 receptor.";
RN J. Biol. Chem. 275:30531-30536(2000).
RP SEQUENCE FROM N.A.
RX MEDLINE=20545741; PubMed=11093801;
RA Nethacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA Clivelli O.;
RT "Molecular cloning and characterization of a second human cysLT2
RT leukotriene receptor: discovery of a subtype selective agonist.";
RL Mol. Pharmacol. 58:1601-1608(2000).
RN 14
RP SEQUENCE FROM N.A.
RA Dunn M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 15
RP SEQUENCE OF 17-346 FROM N.A.
RA Suga H.;
RT "Homo sapiens cysLT2 leukotriene receptor 1 like receptor.";
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysLT2 leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system. Stimulation by BAY u9773, a
CC partial agonist, induces specific contractions of pulmonary veins
CC and might also have an indirect role in the relaxation of the
CC pulmonary vasculature endothelium. The rank order of affinities for
CC the leukotrienes is LTC4 > LTD4 > LTE4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC heart, placenta, spleen, peripheral blood leukocytes and adrenal
CC gland. In lung, expressed in the interstitial macrophages, and
CC slightly in smooth muscle cells.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC
CC EMBL; AB038269; BAB03601.1; -
CC EMBL; AF254664; AAG17281.1; -
CC EMBL; AF279611; AAK69485.1; -
CC EMBL; AL137118; CAC29102.1; -
CC EMBL; AB041644; BAB16379.1; -
CC MIM; 605666; -
CC InterPro: IPR004071; CysLeuk_receptor.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR01533; CysLTRRECEPT.
CC PRINTS: PR00237; GPCR_RHOOPS_N.
CC PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
CC PROSITE: PS50262; G-PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 63 1 (POTENTIAL).
FT DOMAIN 64 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 123 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 144 3 (POTENTIAL).
FT DOMAIN 145 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 174 4 (POTENTIAL).
FT DOMAIN 175 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 5 (POTENTIAL).
FT DOMAIN 226 245 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 266 6 (POTENTIAL).
FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 307 7 (POTENTIAL).

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FT DOMAIN 308 346 CYTOPLASMIC (POTENTIAL).
FT DISULFID 111 187 BY SIMILARITY.
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 346 AA; 39635 MW; EB54A4A2DCE5ED CRC64;

Query Match 27.5%; Score 487.5; DB 1; Length 346;
Best Local Similarity 34.9%; Pred. No. 2.9e-25;
Matches 111; Conservative 64; Mismatches 114; Indels 29; Gaps 10;

QY 23 NCIDENIPKMHYIPVYIGIIFLVGPGNAVISTYIFKRPKMSST---TIMNLACTD 79
DB 30 NCTIEN--FKREFPIYLIIFGVLGNG--LSIYVF--LQPYKSTSVNFMNLAIISD 84
QY 80 LLYLTSPLFIHYAAGENNIFGDMCKFIRESFHPNLYSILFLTCGSIFFRCVLIHPM 139
DB 85 LLIETSLPFRADYILKRSNMFGLACRIMSTSLVNMYSITFLVLSVFLAMVHPF 144
QY 140 SCESIHKRCNAVACAVVWIISLVAVIPMFLITSTNRSACLDLTSDELNTIK-- 196
DB 145 RLHVTISRSAMILGIIIMLIMASST---MLDSSGSEONS---VTSCELEMLYKIAK 197
QY 197 --WNLILATPFCPLVYITLCTYTTIITHTGLQDSCK---QKARILITLLAFY 251
DB 198 LQTMNYIALVVGCLLPFTLSICLLIIRYLKAVESEGSRVSHRRALTTIITLIIF 257
QY 252 VCFPLPHILVYIRIESRLTISCISENOIHEAVYSPRIALNFGNLLYVVSNDNQ 311
DB 258 LCPFLPITLRLVHLTKTKVGL---CKDLKALVITLALANANCFNPLTYFAGENK 314
QY 312 AVCSIVRCKVSGNLEQAK 329
DB 315 RLKSLALR---KGHPQAK 329

RESULT 13
P2Y2_MELGA STANDARD; PRT; 328 AA.
ID P2Y2_MELGA
AC O93361;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN P2Y3.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
ON NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98401046; PubMed=9730913;
LA Li O., Olesky M., Palmer R.K., Harden T.K., Nicholas R.A.;
RT "Evidence that the p2y3 receptor is the avian homologue of the
mammalian p2y6 receptor."
RL Mol. Pharmacol. 54:541-546(1998).
CC - FUNCTION: RECEPTOR FOR EXTRACELLULAR UDP-ADP - UTP. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; AF069555; AAC23863.1;
DR HSSP; P34996; IJDD.

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DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PS00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECPT_FL1; FALSE_NEG.
DR PROSITE; PS50262; G-PROTEIN_RECPT_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 22
FT TRANSMEM 23 43
FT DOMAIN 44 57
FT TRANSMEM 58 78
FT DOMAIN 79 96
FT TRANSMEM 97 117
FT DOMAIN 118 139
FT TRANSMEM 140 160
FT DOMAIN 161 189
FT TRANSMEM 190 210
FT DOMAIN 211 231
FT TRANSMEM 232 252
FT DOMAIN 253 275
FT TRANSMEM 276 298
FT DOMAIN 299 323
FT CARBOHYD 5 5
FT DISULFID 94 172
SQ SEQUENCE 328 AA; 37594 MW; B74D9B95C7164A5 CRC64;

Query Match 27.5%; Score 486.5; DB 1; Length 328;
Best Local Similarity 35.9%; Pred. No. 3.2e-25;
Matches 111; Conservative 55; Mismatches 124; Indels 19; Gaps 8;

QY 16 DYAAFGNCIDENIPKMHYIPVYIGIIFLVGPGNAVISTYIFKRPKMSSTITMNL 75
DB 5 NCTIEN--FKREFPIYLIIFGVLGNG--LSIYVF--LQPYKSTSVNFMNLAIISD 84
QY 76 ACTDLVLTSLPFIHYAAGENNIFGDMCKFIRESFHPNLYSILFLTCGSIFFRCV 135
DB 64 ATADLVVCSPLIIVNTQWDYWPFGDFLTKFVFGQYTNLHGSILFLTISVGRWGI 123
QY 136 IHMPCSESIHK---TRCAVACAVVWIISLVAVIPMFLITST--NRNRSACDLTSD 191
DB 124 CHPLA--SMHKKKKKLTWICAAVWFIVIAQCLP--TFEVSASTGTORNRVTCYDLS 180
QY 192 LNTIKWNLITATPFCPLVYITLCTYTTIITHTGLQDSCK-----KOKARILTI 244
DB 181 SASYPPYIGITLTITLGPFAITLACYSMARIL---CQDELGLAVHKKKDAVAMTI 237
QY 245 LLLAFVYCFPLPHILVYIRIESRLT--SISCSINOIHEAVYSPRIALNFGNLLY 303
DB 238 IVYIVFSTSPFPHILVYIRIESRLT--SISCSINOIHEAVYSPRIALNFGNLLY 297
QY 304 VVSDNFOQA 312
DB 298 FTQRRFRES 306

RESULT 14
P2Y2_RAT STANDARD; PRT; 374 AA.
ID P2Y2_RAT
AC P41232;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
GN P2Y2 OR P2R1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95110548; PubMed=7811468;
LA Rice W.R., Burton F.M., Fiedel D.T.;
RT "Cloning and expression of the alveolar type II cell P2u-purinoergic

```

```

RT      receptor ;
RL      Am. J. Respir. Cell Mol. Biol. 12:27-32(1995).
RN
RP      SEQUENCE FROM N.A.
RC      STRAIN-Wistar; TISSUE-Pituitary;
RA      Chen Z.P., Krull N., Xu S., Levy A., Lightman S.L.;
RL      Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Wistar;
RA      MEDLINE=98099857; Pubmed=9437211;
RA      Seye C.I., Gadeau A.P., Daret D., Dupuch F., Alzieu P., Capron L.,
RA      Desgranges C.;
RT      "Overexpression of P2Y2 purinoceptor in intimal lesions of the rat
RT      aorta.";
RL      Arterioscler. Thromb. Vasc. Biol. 17:3602-3610(1997).
CC      -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC      activate a phosphatidylinositol-calcium second messenger system.
CC      The affinity range is UTP = ATP > ATP-gamma-S > 2-methylthio-ATP
CC      = ADP.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; D09402; AAA61565.1; -
DR      EMBL; L46865; AAB0209.1; -
DR      EMBL; U56839; AAC00048.1; -
DR      HSSP; P34996; 1DDP.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm.1; 1.
DR      PRINTS: PR00237; GPCRHHODPSN.
DR      PROSITE; PS00237; G-PROTEIN_RECPT_P1_1; 1.
DR      PROSITE; PS50262; G-PROTEIN_RECPT_P2_1; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
FT      DOMAIN 1 32
FT      TRANSMEM 33 59
FT      TRANSMEM 60 70
FT      DOMAIN 71 93
FT      TRANSMEM 94 110
FT      TRANSMEM 111 129
FT      TRANSMEM 130 152
FT      TRANSMEM 153 172
FT      TRANSMEM 173 194
FT      TRANSMEM 195 220
FT      TRANSMEM 221 245
FT      TRANSMEM 246 268
FT      TRANSMEM 269 286
FT      TRANSMEM 287 308
FT      DOMAIN 309 374
FT      CARBOHYD 9
FT      CARBOHYD 13
FT      DISULFID 106 183
FT      CONFLICT 132 132
FT      CONFLICT 143 143
FT      CONFLICT 146 166
FT      CONFLICT 188 188
SO      SEQUENCE 374 AA; 42137 MW; 2DA653AA20A1A93 CAC64;

Query Match 27.3%; Score 483.5; DB 1; Length 374;
Best Local Similarity 35.2%; Pred. No. 5.5e-25;
Matches 99; Conservative 56; Mismatches 117; Indels 9; Gaps 2;

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Oy		88	ELIHVASENNITFGDGMKFEIREEPHNTKSILTEFLGCEIFRVCYIIHPMOSFIHKT	147
Dd		88	LIVYYAGDDHMFSTVLCKLVRELFYNLWCSILEFLTCISVHRCGLGVRLSHLSGA	147
Oy		148	RCAVACAAVMYMIISLVAVIPMTFLTSTNFRNSACDLTSSDELNTIKWNLLTFATFE	207
Dd		148	RVARRAAVALVVVLVLAACAQPVLYEFTYTYSRGTRICHTSARELFSHFVAVSMMGLLF	207
Oy		208	CLEPLVTLCVYTTTIHTL-----THGLOTDSCLKOKARLTILLALLAFYCVCFPIHLR	261
Dd		208	AVPESILTVCYVLMARRLLKPAYGTGPLR---AKRSVRIALVLAENFALCFPIHVTR	264
Oy		262	VIRIESRLISTSCSIENOHEMYIYSRPLAINTGNLLY	302
Dd		265	TLYSFERSLDLSCHTLNAINMAVKITRPASANSCLDPVLY	305
<p>RESULT 15 P2Y2_MOUSE</p>				
ID	P2Y2_MOUSE	STANDARD:	PRT;	373 AA.
AC	P35383; 009031; G9CPZ4;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, last sequence update)			
DT	15-JUN-2002 (Rel. 41, last annotation update)			
DE	P21 purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)			
DE	(Purine-glyc receptor).			
GN	P2RY2 OR P2RU1.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93281707; PubMed=7685114;			
RT	Lustig K.D., Shlau A.K., Brake A.J., Julius D.;			
RT	"Expression cloning of an ATP receptor from mouse neuroblastoma			
RT	cells.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:5113-5117(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96316177; PubMed=87939319;			
RT	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RT	Akaiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RT	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana R.;			
RT	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochua H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schirral L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustinich S., Hill D., Hofman M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyokawa K., Wang K.H., Weltz C., Whitaker C., Wilming L.,			
RA	Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontseki S.,			
RA	Hayashizaki Y.;			
RA	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUB=Breast tumor;			
RA	Straussberg R.;			

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP MUTAGENESIS OF LYS-107; ARG-110; HIS-262; ARG-265; LYS-289 AND
ARG-292.
RX MEDLINE-95181393; PubMed-7876172;
RA Erb L., Garrard R.C., Wang Y., Quinn T., Turner J.T., Weisman G.A.;
RT "Site-directed mutagenesis of P2U purinoreceptors. Positively charged
amino acids in transmembrane helices 6 and 7 affect agonist potency
and specificity.";
RL J. Biol. Chem. 270:4185-4188(1995).
CC -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
activate a phosphatidylinositol-calcium second messenger system.
CC The affinity range is UTP > ATP > ATP-gamma-S >> 2-methylthio-ATP
CC = ADP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: SPLEEN, TESTIS, KIDNEY, LIVER, LUNG, HEART AND
CC BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; L14751; AAA39871.1; -;
DR EMBL; S83099; AAB50735.1; -;
DR EMBL; AK005013; BAB23746.1; -;
DR EMBL; AK017378; BAB30719.1; -;
DR EMBL; BC006613; AAH06613.1; -;
DR HSSP; P34996; 1DD.
DR MGD; MG1:105107; P2Y2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1;
DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT DOMAIN 60 70
FT TRANSMEM 71 93
FT DOMAIN 94 110
FT TRANSMEM 111 129
FT DOMAIN 130 152
FT TRANSMEM 153 172
FT DOMAIN 173 194
FT TRANSMEM 195 220
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FT TRANSMEM 247 269
FT DOMAIN 270 287
FT TRANSMEM 288 309
FT DOMAIN 310 373
FT CARBOHYD 9
FT CARBOHYD 13
FT DISULFID 183
FT MUTAGEN 107 107
FT MUTAGEN 110 110
FT MUTAGEN 262 262
FT MUTAGEN 265 265
FT MUTAGEN 289 289
FT MUTAGEN 292 292
FT CONFLICT 17 17
FT CONFLICT 120 120
FT CONFLICT 125 125
FT CONFLICT 196 196
FT CONFLICT 263 263
FT CONFLICT 355 355
FT CONFLICT 369 371
SQ SEQUENCE 373 AA; 42174 MW; 590BBE502E41B3AE CRC64;

Query Match 27.0%; Score 479; DB 1; Length 373;
Best Local Similarity 34.4%; Pred. No. 1.le-24;
Matches 97; Conservative 58; Mismatches 117; Indels 10; Gaps 2;
QY 28 NIPLKMYLPVYIGIIFLVGPPGNAVISTYIFKRPKSSITIMLNACTDLYLSLP 87
DB 28 NEDFYVLLPVSYGVCVGLCLNVVALYIFLCRLKTNASTYWFHLAVSDSYAASLP 87
QY 88 FLIHVYASGEMWIFGDFPKCFRFSFHNLSSTILECFSPFRVCIHMSQFSIKT 147
DB 88 LLVYIYANGDMPPSTVYCKLVRFLEYNLCSTILEFCISVHRCGLVRFPHSIRMGRA 147
QY 148 RCAYVACAVVMIISLVAVIPMTFLITSTNRTRSACDLTSSDELNTIKMYNLTATTE 207
DB 148 RYARVAVVWVVLVACQAPVLYFTSVRGTRITCHDTSARELFSEHVAVYSVWGLLE 207
QY 208 CLPLVIVLYCTTTIHTL-----THQLQDSCLEKQARLTIILLAFVYCLPHIL 260
DB 208 AVPSVYIIVCYVLARRLKPKAYGTGGLPR--AKRSVSTIALVLAVALCELPFHYT 264
QY 261 RVIRIESRLSISCSIEHQIHEAYIVSRPLAALNTPGRLLY 302
DB 265 RTLYVSFRSLDSCHTILNAINMAYKITRPLASANSCLDPVLY 306

Search completed: May 30, 2003, 13:45:04
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:42:28 ; Search time 40 Seconds

(without alignments)
809.933 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVSGNLBOAKKISYNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR-73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	32.0	373	2	JC4737
2	565.5	31.9	362	2	S33733
3	562	31.7	373	2	JC4162
4	514	29.0	365	2	S68679
5	479	27.0	373	2	A47556
6	438	24.7	375	2	A54946
7	423	23.9	328	2	I55450
8	419.5	23.7	420	2	I51667
9	405	22.9	328	2	JC4800
10	397	22.4	427	2	S17148
11	396.5	22.4	432	2	A43448
12	388.5	21.9	399	2	I48705
13	388.5	21.9	425	2	A37912
14	380	21.5	308	2	I50241
15	376.5	21.3	361	2	B45680
16	376.5	21.3	397	2	S66518
17	370	20.9	355	2	G02436
18	356	20.1	383	2	S55594
19	355	20.0	352	2	G00048
20	354	20.0	352	2	A45747
21	353	19.9	362	2	S68207
22	353	19.9	362	2	B57641
23	349.5	19.7	423	2	JC7677
24	349	19.7	356	2	S42096
25	348	19.6	354	2	I53033
26	348	19.6	362	2	A57641
27	347.5	19.6	363	2	A49092
28	346.5	19.6	344	2	T09508
29	345.5	19.5	363	2	I48261

30	344.5	19.5	378	2	B55735	lymphocyte-specific
31	344	19.4	353	2	JC2492	G protein-coupled
32	340	19.2	370	2	JC5549	hepatic p2y5-
33	339.5	19.2	363	2	JC2543	angiotensin II rec
34	339	19.1	360	2	G02064	G protein-coupled
35	338.5	19.1	359	2	S15403	angiotensin II rec
36	337	19.0	353	2	S28787	neuropeptide Y/pep
37	336.5	19.0	360	2	A53611	interleukin-8 rece
38	336	19.0	362	2	JN0694	angiotensin II rec
39	334	18.9	356	2	I49340	MIP-1 alpha recept
40	332.5	18.8	355	2	JQ1231	chemokine (C-C) re
41	328	18.5	355	2	A45177	G protein-coupled
42	327	18.5	355	2	JC5067	G protein-coupled
43	327	18.5	387	2	I69202	G protein-coupled
44	326.5	18.4	378	2	A45680	angiotensin II rec
45	325.5	18.4	359	2	S44425	

ALIGNMENTS

RESULT 1

JC4737

G protein-coupled receptor p2y1 - human

N:Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C:Accession: JC4737; JC4615; S54253

R:Janssens, R.; Commun, D.; Piroton, S.; Samson, M.; Boeynaems, J.;

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A:Title: Cloning and tissue distribution of the human P2Y1 receptor.

A:Reference number: JC4737; MUID:96205320; PMID:8630005

A:Accession: JC4737

A:Molecule type: DNA

A:Residues: 1-373 <JAN>

A:Cross-references: GB:S81950; NID:q1839438; PIDN:AA847091.1; PID:q1839439

R:Ayanathan, K.; Webb, T.E.; Sandhu, A.K.; Achwal, R.S.; Barnard, E.A.; Kunapuli,

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A:Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A:Reference number: JC4615; MUID:96158962; PMID:8579591

A:Accession: JC4615

A:Molecule type: mRNA

A:Residues: 1-373 <AVY>

A:Cross-references: GB:U42029; NID:q1147730; PIDN:AA97872.1; PID:q1147731

A:Experimental source: erythro leukemia cells

R:Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.

Submitted to the EMBL Data Library, May 1995

A:Description: Cloning of a human putative P2Y receptor.

A:Reference number: S54253

A:Accession: S54253

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137,139-373 <LEO>

A:Cross-references: EMBL:249205; NID:q798835; PIDN:CAA89066.1; PID:q798836

C:Comment: This receptor belongs to a family of G protein-coupled receptors. It resp

C:Genetics:

A:Gene: p2y1; GDB:p2y1

A:Cross-references: GDB:677125; OMIM:601167

A:Map position: 3pter-3qter

C:Superfamily: ATP receptor P2U

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane i

F:52-77/Domain: transmembrane #status predicted <TM1>

F:88-111/Domain: transmembrane #status predicted <TM2>

F:124-152/Domain: transmembrane #status predicted <TM3>

F:171-191/Domain: transmembrane #status predicted <TM4>

F:214-237/Domain: transmembrane #status predicted <TM5>

F:261-282/Domain: transmembrane #status predicted <TM6>

F:305-328/Domain: transmembrane #status predicted <TM7>

F:11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status pre

F:330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre

F:343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin i

[illegible]

RESULT 5
A47556
ATP receptor P2u - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47556
R:Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells
A:Reference number: A47556; MID:93281707; PMID:7685114
A:Accession: A47556
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <LDS>
C:Cross-references: GB:114751; NID:3309457; PIDN:AAA39871.1; PID:9309458
C:Superfamily: ATP receptor P2u
;Keywords: transmembrane protein

[illegible]

RESULT 6
A54946
P-2U nucleotide receptor - human
C:Species: Homo sapiens (man)
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C:Accession: A54946
C: Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarewski, E.R.; Burch, L.H.; Olsen, J.C.

```

Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A:Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cys
A:Reference Number: A54946; MUID:94211846; PMID:8159738
A:Accession: A54946
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-375 <PAR>
A:Cross-references: GB:007225
A>Note: parts of this sequence were confirmed by protein sequencing
C:Genetics:
A:Gene: GDB:P2RY2; HP2U; P2U
A:Cross-references: GDB:362713; OMIM:600041
A:Map position: 11q13.5-11q14.1
C:Superfamily: ATP receptor P2U
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      24.7%; Score 438; DB 2; Length 375;
Best Local Similarity 33.0%, Pred. No.2,1e-30;
Matches 93; Conservative 59; Mismatches 118; Indels 12; Gaps 4;

QY    28 NIPKMYLPVIGIIFLVGFPGNAAVVISYIFKMPWKSSTIIMLACTDLITYTSLP 87
       |   ||| ||| : : : : : : : : : : : : : : : : : : : : :
Db     28 NEDKRVLLPYSYGVVCVLGLCLNAVGLYFLCKRLKWNASTYTMFHLAVSDALYASLP 87

QY    88 FLHYVASGEWMIGDGMCKFIRESFHNLYSILTFPTCFSEFFRYCVIIHMSCFSIHKT 147
       |   ||||| YARGDHMPSTYLCKLVRFLEFTNLKCSILFELTCISVHRCGLGRLSRLNGRA 147
Db     88 LLYVIYARGDHMPSTYLCKLVRFLEFTNLKCSILFELTCISVHRCGLGRLSRLNGRA 147

QY    148 RCAYVACAAVMWISLVAVVIPTEFLTISTNRTNRSGACLDLTSSDELNTIKWNIILTATFE 207
       |   ||| : : : : : : : : : : : : : : : : : : : : :
Db     148 RYARVAGVAWVLLLAQAAPVLYFVTLSAR -GPLTCHDTSAPELFSRFVAVSSVMGLLF 206

QY    208 CLPLVIYTLCTTYTHHL-----THGLQTSCLKOKARKRLITLLLLAFVQCFLPHIL 260
       |   :: :|| : : : : : : : : : : : : : : : : : : : : :
Db     207 AVPRAVLIYCVLMARLRKLPRAYGTSGGLPR--AKRKSVRTIAVLAVALCPHPHYT 263

QY    261 RVIRIESRLNISCSIENOIHEAVYISRPALALTFCNILL 302
       |   | : : : : : : : : : : : : : : : : : : : : :
Db     264 RTLYYSFRSLDLSCHTTNALMAKYVR-LASANSCLDPVLY 304

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RESULT 7
155450
G protein-coupled P2 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence-revision 02-Jul-1996 #text-change 19-May-2000
C:Accession: 155450
R:Chang, K.; Hanaka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A:Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor
A:Reference number: 155450; MUID:96064682; PMID:7552819
A:Accession: 155450
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-328 <RES>
A:Cross-references: GB:053665; NID:g1066007; PIDN:BA09816.1; PID:g1066008
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor

	Query Match	23.9%	Score 423;	DB 2:	Length 328;
	Best Local Similarity	32.9%;	Pred. No. 3.7e-29;		
	Matches	96;	Conservative 44;	Mismatches 126;	Indels 26; Gaps 5
Qy	36 LPVYIGIIELVGPEPNNAVVISPIRKMRWKSITIMLACTDILLYLTSPFLHYVAS	95			
	: : : :	:	: : : :		
Db	29 LPPVSYVLNVGLPNTNCVIAOICASRRLFRSAVYTLLALADLIYACSLPLLNYNAR	88			
Qy	96 GENNIIFGDMEKFIREFSFENLYSILFETCFISIRYCVIIHPMSOFSIHK--TRCAVY	152			
	: : : : : : : :	:	: : : :		
Db	89 GDHVPFGDLACLRYLFLEYANLHGSIILFTICISFYRGIGICHPAPW--HKRGGRRAAY	146			
Qy	153 ACAVWIISLVAVINMTFLISTNTKNTNSACCLDISSDELNITKKYNLLTATTPOLPLV	212			
	: : : :	:	: : : :	:	: :

Db 147 VCGVWLVVTAQCLPFAVFAATGIGRNFTVCYDLSPPILSTRYLPYGMALTVIGFLPEFT 206
 Qy 213 IVTLCTYTIHTLHGLQTDSC-----LKOKARRLTLLLLAFYVCELPFHIL 260
 Db 207 ALLACYCRMARRL-----CRDDGPAQVPAQERSRAANAAVVAVVAVFISLPEPHIT 258
 Qy 261 RVVIESRL-SIGCSINQIHEAYISRPALANTGNLLLYVVSDFNQ 311
 Db 259 KTAVALAVNSPQVSCPVLETFPAAYKGRFPASANSVLDPLTFYFTQCKFR 310

RESULT 8

151667
 thrombin receptor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: 151667

R:Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanavicz, T.; Turck, C.W.; Vu, T.H.; C

Nature 368, 648-651, 1994.

A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac

A:Reference number: 151667; MUID:94195429; PMID:8145852

A:Accession: 151667

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-420 <GER>

A:Cross-References: EMBL:U09632; NID:9495197; PIDN:AAAL8498.1; PID:9495198

Query Match 23.7%; Score 419.5; DB 2; Length 420;
 Best Local Similarity 31.1%; Pred. No. 9,66-29;
 Matches 93; Conservative 73; Mismatches 108; Indels 25; Gaps 7;

Qy 35 YLPIVYGIIFLVGPGNAVISTYIFKMRPKSSTIIMLACDLYLTSPLPHIYA 94
 Db 103 FVSPILYVVEVIGPLMLLIIIFLKMKYKPAVVMALADIVFVSLPKPIAHIL 162
 Qy 95 SGEMWINGDEPKCKIRSFHNLKSLIFLCFSIFRCVYIIHMSCESHKTKCAVYAC 154
 Db 163 SGNDMLFGPGKCRIVTALFYCNMYCSVLLASISVDRPLAVVPMHSLSMPTMSRAYAC 222
 Qy 155 AVWIIISLVAVIPMTFLTSTNTRNSACLDLTSDELNTIK---WYNLILATTFCL- 209
 Db 223 SFWILISIASPIPLV---TEQTKIPRLDITICHVLDKLDKDF--IYFSSRCLL 276
 Qy 210 ----PLVIVLCYTTIHTLHGLQTDSCQKARRLTLLLLAFYVCELPFHILYIRI 265
 Db 277 FFEVPIITTYIGIIRSLSSSIENSCKKTRALLAVVLCVFIICFPTNVL----- 331
 Qy 266 ESRLISCSINQIHEAYISRPALANTGNLLLYVVSDFNQAVCTVRC-IYS 322
 Db 332 ---FLTHYLOEANEFLYFAILSACVGSVSCCLDPLIYYASVOCQRYLSLCCRVVS 387

RESULT 9

151667

P2Y6 receptor - human

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C:Accession: J04800; G02514

R:Communi, D.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 222, 303-308, 1996

A:Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept

A:Reference number: J04800; MUID:96222498; PMID:8670200

A:Accession: J04800

A:Molecule type: mRNA

A:Residues: 1-328 <CON>

A:Cross-References: EMBL:X97058

A:Experimental source: Placenta

R:Hammett, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.

submitted to the EMBL Data Library, March 1996

A:Reference number: H01373

A:Accession: G02514

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 'W',4-328 <HAM>
 A:Cross-References: EMBL:U52464; NID:91407632; PIDN:AA03572.1; PID:91407633
 C:Genetics:
 A:Gene: P2Y6
 C:Superfamily: ATP receptor P2u
 C:Keywords: glycoprotein; placenta; receptor; transmembrane protein
 F:26-52/Domain: transmembrane #status predicted <TM1>
 F:63-86/Domain: transmembrane #status predicted <TM2>
 F:104-122/Domain: transmembrane #status predicted <TM3>
 F:143-167/Domain: transmembrane #status predicted <TM4>
 F:193-216/Domain: transmembrane #status predicted <TM5>
 F:241-264/Domain: transmembrane #status predicted <TM6>
 F:283-305/Domain: transmembrane #status predicted <TM7>
 F:5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.9%; Score 405; DB 2; Length 328;
 Best Local Similarity 32.6%; Pred. No. 1,36-27;
 Matches 94; Conservative 44; Mismatches 140; Indels 10; Gaps 4;

Qy 32 KMAYLPVYGIIFLVGPGNAVISTYIFKMRPKSSTIIMLACDLYLTSPLPHI 91
 Db 25 KOLLPPVYSAVLAAGPLNLCVYIQCTSRRLTRAVVTLADLLYACSLPLIY 84
 Qy 92 YVASEGWIREDPKCKIRSFHNLKSLIFLCFSIFRCVYIIHMSCESHK---TR 148
 Db 85 NYAGDHPFEDFCACRVLRFLYANLHGSILFLCFSIFRCVYIIHMSCESHK--- 142
 Qy 149 CAVACAVWIIISLVAVIPMTFLTSTNTRNSACLDLTSDELNTIKMYLITATTF 208
 Db 143 AAMLVCAVWLAVALTQCLPFAIFAATGIGRNFTVCYDLSPPALATHMPGALTIVGFL 202
 Qy 209 LPLVIVLCYTTIHTLHGLQTDSCQKARRLTLLLLAFYVCELPFHILYIRI 264
 Db 203 LPFAALACVCLLACRLCRDQGPAPVPAQERGRKAAVVAVVAVFISLPEPHIT 262
 Qy 265 IESRL-SIGCSINQIHEAYISRPALANTGNLLLYVVSDFNQ 311
 Db 263 LAVSTPGVPCVLEAFPAAYKGRFPASANSVLDPLTFYFTQCKFR 310

RESULT 10

alpha-thrombin receptor - Chinese hamster

C:Species: Citellus griseus (Chinese hamster)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S17148

R:Rasmussen, U.B.; Youret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavir

FEBS Lett. 288, 123-128, 1991

A:Title: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to

A:Reference number: S17148; MUID:91348247; PMID:1652467

A:Accession: S17148

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-427 <RAS>

A:Cross-References: EMBL:X61958; NID:9940495; PIDN:CAAA3957.1; PID:949538

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.4%; Score 397; DB 2; Length 427;
 Best Local Similarity 28.4%; Pred. No. 8,76-27;
 Matches 95; Conservative 75; Mismatches 141; Indels 24; Gaps 6;

Qy 10 NASDFPDYAAFGNCTDENIPLKMH-----YLPVYGIIFLVGPGNAV 53
 Db 65 NESFLPEGRAIYLNKSHSPAPLAFISEDAGYLTSPMLRLFLPSVTFEVVSLPLNLL 124
 Qy 54 VISTYIRKMRPKSSTIIMLACTDLYLTSPLPHIYVASEGNMTFGPMCKIRFSF 113
 Db 125 AIAVEVLMKRVKPAVVMYMLAMADLVFVSLPLKISYFSGSDWQFGSGMCRFATAP 184
 Qy 114 HFNYSILFLTFESIFRCVYIIHMSCESHKTRCAVACAVWIIISLVAVIPMTFLT 173
 Db 185 YCNMTASIMLTATISIDRLAVVYPIQSLSWRLGRANFTCLIVYVMAINGVPL-LIKE 243

Db 281 VPLISTVCYVSIIRCLSSAVANRSKSRALFLSAAFICFIITICFETNLLTAHYS-- 338
 Oy 269 LLSICSIENQIHEAYISRPLALNTEGNTLLVYVSDNQAVCSYVRCK----- 320
 Db 339 FLSHTSTTE-NAIRALYLCVCVSSISCIIDPLIYVYVSECCRYVSYILCKESSDPSSY 397
 Oy 321 -VSGNLEQAKKISYSNN 336
 Db 398 NSSGQLMASKMDTCSSN 414

RESULT 14

150241
 G:protein-coupled receptor 6H1 - chicken
 N:Alternate names: purinoceptor 6H1
 C:Species: Gallus gallus (chicken)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
 C:Accession: 150241; J04618
 R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
 J:Immunol. 151, 628-636, 1993
 A:Title: Identification of a G protein coupled receptor induced in activated T cells.
 A:Reference number: 150241; MUID:9332058; PMID:8393036
 A:Accession: 150241
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-308 <KAP>
 A:Cross-references: GB:J06109; NID:9304383; PIDN:AA06587.1; PID:9304384
 R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
 Biochem. Biophys. Res. Commun. 219, 105-110, 1996
 A:Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
 A:Reference number: J04618; MUID:96190677; PMID:8619790
 A:Accession: J04618
 A:Molecule type: mRNA
 A:Residues: 1-308 <MEB>
 A:Cross-references: GB:J06109; NID:9304383; PIDN:AA06587.1; PID:9304384
 A:Experimental source: T-cells
 C:Comment: This receptor plays a role in T-cell activation.
 C:Genetics:
 A:Gene: p2Y5
 C:Superfamily: ATP receptor P2u
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:15-40/Domain: transmembrane #status predicted <TM1>
 F:51-74/Domain: transmembrane #status predicted <TM2>
 F:89-109/Domain: transmembrane #status predicted <TM3>
 F:133-153/Domain: transmembrane #status predicted <TM4>
 F:177-201/Domain: transmembrane #status predicted <TM5>
 F:227-248/Domain: transmembrane #status predicted <TM6>
 F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 21.5% Score 380; DB 2; Length 308;

Best Local Similarity 30.8%; Pred. No. 1.8e-25;
 Matches 90; Conservative 58; Mismatches 134; Indels 10; Gaps 6;

Oy 23 NCNDENPLKMHLPVYIGIIFLVGPGNAVISTYIFKAPKMSSTIIMNACTDLY 82
 Db 5 NCSFED-SFRTYLYGCVFVGLANCAIYIFFTLKVRNETTYMNLAIIDL 63
 Oy 83 LLSIPFLIHYASGENMIFGDMCKEIRFSFHELYSLILFCESIFRCVITIHPSCE 142
 Db 64 VFLPFRITTYFV-RNMPEDVLCISVTLFYTNMYSILFLICISYDRFLAYHPRSK 122
 Oy 143 SIHKTRCAVAVAVIISLVAIIPMTFLTSTNRTNSACLDLTSSDELNTIKW---- 198
 Db 123 TLRTKRARIYCAVAVITVLAGSPASF-POSTNRQNTTEORCFENPESTWKTYSRI 181
 Oy 199 NLLIFATPCLPLVYILCTTIIHTLH--GLQDSCLOKARRLTILLAFYVFLP 256
 Db 182 VIFIEIVGFPIPLNLTCTSTVLRNLKRLTLSSRNKLSKKVLMKIFVHIVFCFCVP 241
 Oy 257 FHLIRVIRISRLIS-ISCSEIENQIHEAYISRPLALNTEGNTLLVYVSD 307
 Db 242 YNTLLIYSIMRTQWINCSTVAVRTMYPVTLICIAVSNCCFDEIVYFTSD 293

RESULT 15

B45680
 G:protein-coupled peptide receptor EBI 2 - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: B45680
 R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
 J:Virol. 67, 2209-2220, 1993
 A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
 A:Reference number: A45680; MUID:93188173; PMID:8363238
 A:Accession: B45680
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-361 <BIR>
 A:Cross-references: GB:L08177; NID:9292056; PIDN:AAA3924.1; PID:9292057
 A:Experimental source: B-lymphocytes
 A:Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBI:127097)
 C:Superfamily: ATP receptor P2u
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.3% Score 376.5; DB 2; Length 361;

Best Local Similarity 26.9%; Pred. No. 4.3e-25;
 Matches 92; Conservative 70; Mismatches 159; Indels 21; Gaps 7;

Oy 11 ASDP-PDYAAFGNCTDENIPDKMY-----LPVYIGIIFLVGPGNAVISTYIFKMR 63
 Db 6 ANNTTPSATPQSGNDP-----LVNHSSTARVPLHSLVFIIGVGNLALVYIQNRK 61
 Oy 64 PKMSSTIIMNACTDLYLTSLEPLIHYASGENMIFGDMCKEIRFSFHELYSLILF 123
 Db 62 KINSTTLYSNLVSDILFTTALPTRIAYYAMGPDNRIGDALCRITAVEYINTYAGVNF 121
 Oy 124 LTCFSIRYCVIITHMPCFSGIHKTRCAVAVAVIISLVAIIPMTFLTSTNRTNSAC 183
 Db 122 MTCLSIDRFVAVVHPLVYKIRLEHAKGVCIFWMLVPAQOTPLPINPSKQDAERTTC 181
 Oy 184 LDLTSSDELNTIKWNLILATTECLPLVITLCTYTIHTL-----THGIQDSCLOK 238
 Db 182 MEYVNFETKSLPILLGACFIVPLIILICYSIQCKLRTAKONPLEKSGVNRK 241
 Oy 239 ARRLTILLAFYVCEPLPHILVIRIESRLISCSIF-NOIHEAYISRPLAALNTFG 297
 Db 242 ALMTIILIIIVFVLCFPHYV-AIIQHMIRKLFESNLFESQHSRFSISLHFTVCLMNF 300
 Oy 298 ---NLLYVVSNDQOAVCSYVRCKVSGMLEAKKISYSNN 336
 Db 301 CNDPFLYFRACKGYKRWMLKROVSVISSAVKAPREN 342

Search completed: May 30, 2003, 13:47:20
 Job time: 42 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: May 29, 2003, 23:40:20 ; Search time 1706 Seconds

(without alignments)
3199.226 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPDIYLANASDFPDYAA.....RCVSGNLEQAKKISYNNP 337

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame-p2n.model -DEV=ylh

-Q=/cgn2.1/USPTO.spool/US1002775/runat_23052003_160018_12459/app.query.fasta_1.519

-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0

-UNIT5-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45

-DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US1002775 @CGN 1.1 1906 @runat_23052003_160018_12459 -NCPU=6 -ICPU=3

-NO_MAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONKLOC

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_estl:*

10: gb_estl2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	478	27.0	2542	11	AK017378	AK017378 Mus muscu
2	478	27.0	3001	11	AK005013	AK005013 Mus muscu
3	400	22.6	744	14	BM723768	BM723768 UI-E-E01-
4	399	22.5	956	17	CNS028Y4	AL186585 Tetradon
5	399	22.5	1101	17	CNS04VW3	AL109578 Tetradon
6	395.5	22.3	3005	14	AK019478	AK019478 Mus muscu
7	388	21.9	623	14	B0038875	B0038875 pgn1c.pk0
8	371.5	21.0	821	14	BM946831	BM946831 UI-M-EH0P
9	370.5	20.9	2020	11	BC013202	BC013202 Homo sapi
10	370	20.9	971	9	AU091121	AU091121 AU091121
11	367.5	20.8	946	9	AL551903	AL551903 AL551903
12	366.5	20.7	904	9	AL532537	AL532537 AL532537
13	366.5	20.7	931	9	AL547762	AL547762 AL547762
14	353	19.9	641	14	B0396255	B0396255 NISC.ng19
15	352	19.9	638	9	AL675845	AL675845 AL675845
16	348	19.6	1101	17	CNS0532S	AL18925 Tetradon
17	336.5	19.0	1739	11	AK008997	AK008997 Mus muscu
18	334.5	18.9	789	12	BG205056	BG205056 RST24475
19	334	18.9	765	13	B183645	B183645 UNL-P-FN-
20	333	18.8	734	13	BG914321	BG914321 602810633
21	332.5	18.8	851	13	B183118	B183118 603090834
22	331	18.7	1051	13	BM545259	BM545259 AGENCOURT
23	330.5	18.7	1026	17	CNS051MY	AL317059 Tetradon
24	323.5	18.3	613	9	AL657842	AL657842 AL657842
25	321.5	18.2	1063	14	BM918491	BM918491 AGENCOURT
26	319.5	18.0	861	13	B1768868	B1768868 603057774
27	319.5	18.0	1088	13	BM549799	BM549799 AGENCOURT
28	319.5	18.0	1766	11	AK008952	AK008952 Mus muscu
29	318.5	18.0	606	17	AZ953874	AZ953874 2M0219117
30	318.5	18.0	663	13	BM426517	BM426517 pfgf2n.pk0
31	317	17.9	2146	11	BC027965	BC027965 Homo sapi
32	315	17.8	884	12	BG182330	BG182330 RST1196 A
33	311	17.6	938	17	CNS04SUP	AL305672 Tetradon
34	311	17.6	1048	11	AK011967	AK011967 Mus muscu
35	309.5	17.5	1063	14	BM920158	BM920158 AGENCOURT
36	309	17.4	620	13	B1961697	B1961697 MONO1.3.D
37	307	17.3	1074	14	BM917063	BM917063 AGENCOURT
38	306	17.3	989	17	CNS03C14	AL237227 Tetradon
39	305	17.2	808	9	AJ456719	AJ456719 AJ456719
40	303	17.1	741	9	AJ453402	AJ453402 AJ453402
41	302.5	17.1	766	9	AJ450835	AJ450835 AJ450835
42	301	17.0	876	13	B1906283	B1906283 603063222
43	300.5	17.0	1076	14	BM923028	BM923028 AGENCOURT
44	299	16.9	800	9	AJ452624	AJ452624 AJ452624
45	299	16.9	885	9	AL546894	AL546894 AL546894

ALIGNMENTS

RESULT 1
AK017378
LOCUS
DEFINITION
AK017378 2542 bp mRNA linear HTC 19-JAN-2002
library: clone:5430432J15; putative receptor p2y, G-protein
coupled 2, full insert sequence.

ACCESSION
AK017378
VERSION
AK017378.1 GI:12856588
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
clone:lib:RIKEN full-length enriched mouse cDNA library
clone:5430432J15.

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source
1..744
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EO1-alc-9-16-0-UI"
/clone_lib="UI-E-EO1"
/issue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t
ORIGIN

Alignment Scores:

Pred. No.: 1.59e-33 Length: 744
Score: 400.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.59% Indels: 0
DB: 14 Gaps: 0

US-10-023-775b-2 (1-337) x BM723768 (1-744)

QY 258 HIIIELEUARYAIIIEARGLIEGUSEHARGLEULESERIESYSSRIIEGLU 277
|||||
DB 1 CATACCTTAGGCTCATTCGATCGAATCTCGCTTCATCATCGTTCCATTTGAG 60
QY 278 AAGNIIIEHISGLUATYRIIEVALSERATPROLEUALALAEUANSRHPHEGLY 297
|||||
DB 61 AATCAGATCCATGACCTTACATCGTTTACACCTTACGCTCTGACACCTTTGGT 120
QY 298 AenleuleuLeuTyriValValValSerAspAspPheGlnGlnAlaValCysSerThrVal 317
|||||
DB 121 AACCTGTACTATATGTGTGGTGCAGCAGCACTTGCACAGCGCTGCTGCACAGTG 180
QY 318 ArgGysLysValSerCysLysLeuGlnGlnAlaLysLysIleSerTySerAsnPro 337
|||||
DB 181 AGATGCAAGTAAGCGGAGCACTTGAGCAAGCAAAATAATTACTCAACAACCCCT 240

RESULT 4

CNS028Y4/c

LOCUS

DEFINITION

956 bp DNA linear GSS 12-MAY-2000

Tetradon nigriviridis genome survey sequence PUC-ori end of clone

245bp of library G from Tetradon nigriviridis, genomic survey

sequence.

AL186565

GI:7824669

GSS: genome survey sequence.

Tetradon nigriviridis

ORGANISM

REFERENCE

AUTHORS

Bernot,A., Fizames,C., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,

Roest-Crolius,H., Wincker,P., Brothier,P., Quetier,F.,

Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using

Tetradon nigriviridis DNA sequence

JOURNAL

2 (bases 1 to 956)

Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,

Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and

Weissenbach,J.

Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetradon nigriviridis

Unpublished

3 (bases 1 to 956)

Genoscope.

Direct Submission

Submitted (12-APR-2000)

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetradon nigriviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/tetradon.

location/Qualifiers

1..956

/organism="Tetradon nigriviridis"

/db_xref="taxon:99883"

/clone="245p17"

/clone_lib="G"

/note="Genoscope sequence ID : C0AG245CH09SP1-end ;

PUC-ori"

BASE COUNT 251 a 214 c 290 g 176 t 25 others

ORIGIN

Alignment Scores:

Pred. No.: 3.03e-33 Length: 956
Score: 399.00 Matches: 101
Percent Similarity: 51.55% Conservative: 65
Best Local Similarity: 31.37% Mismatches: 129
Query Match: 22.53% Indels: 27
DB: 17 Gaps: 10

US-10-023-775b-2 (1-337) x CNS028Y4 (1-956)

QY 4 PROLEUASPTYLEUAAASNAISERASPEHPCASPTYRIALALAEHAGHEGLY--- 22
|||||
DB 943 CCCCTACCTTTCTT-----CCCTGTGTGTCCCTCTTCTTCTCT 902
QY 23 -----ASGYSYTHASPGUASNIIIEPROLEULYSMETHISTYRIEUPROVAL 38
|||||
DB 901 TCAAGCTGATATATTGATCAAAATCGATGCTTACTGAGAGTACTTCCGCCACCC 842
QY 39 ILETYGLYIIETIEHELEUVALGYPHEPROGLYASNAIYALVAILLESERTHYR 58
|||||
DB 841 TTCTACGGTGTGAGAGTTCGCCGCGTTTCCCGGACCTGTGGTGTCTTCTTGGTTAC 782
QY 59 IIEPHELYMETATRGPTTRIPLYSSERTHYRIIELEMETLEUASNULEUALCYSTHR 78
|||||
DB 781 ATATTGCTTGCACAGTGTGCAGACCTGCATATCTACTCTTCAACCTGGCGCTCA 722
QY 79 ASPLEULEUTYRIEULHUSERLEUPROHELEULIIEHISTYTRYRLASERGLYUAN 98
|||||
DB 721 GACCTGTGTCTCTGCSAGCGCGACCTCTCTTACCTGCACCAACACAGTGG 662
QY 99 TPIIEPHEGLYASPEHMETCYSLYSPHEIIEARPHESERPHESISPHEASNULEUTYR 118
|||||
DB 661 ----CTAAACAGTCCCTTCTGTCATCGCCACACCGCTATCTGTGACGCAACCTTAC 605
QY 119 SERSERIIELEUPHEUTHYRSCYSPHEIRIIEPHEARYR-CYSVALIIEHISPR 138
|||||
DB 604 TCTTCATCTCTTCTGATGTTGGCGACAGCAGCCGCTACTCTGCTGTGAGCAGCC 545
QY 138 OMETSERCYSPHESEIRIIEHISLYSTHRARGYSALAVAILALACYSALAVAILYR 158
|||||
DB 544 GACGCGGAACACTACTGCTGAACCGGCGGGGAGTGTGGTGDACGAGCTGAGCTG 485
QY 158 PILEIIESEIRIEUVALIYALVAILLEPRO--METHRPHLEULEIETHRSETHRASNR 177

RLKSKWVCITIWMAALAPPELLIYSAVSESGEISACTMYTPDKNAKLASAILIK
 VTLFEPFMWAFRCYTIIHTILOAKSSSHKILKYITVLAYINSQFPYNLSIV
 OADVAAMFIENGTISTNIDICPOVTOTLIAFSHCINLVLYFGERRRDLVNTLKN
 LGCTSQAWMVSFTREGSLKSMLLETTGALSIL"
 2981..2986
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 /note="putative"
 polyA_site
 3005
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 /note="putative"
 BASE COUNT 814 a 734 c 648 g 809 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4,36e-32 Length: 3005
 Score: 395.50 Matches: 98
 Percent Similarity: 51.34% Conservative: 74
 Best Local Similarity: 29.25% Mismatches: 150
 Query Match: 22.33% Indels: 13
 DB: 11 Gaps: 8

US-10-023-775B-2 (1-337) x AK019478 (1-3005)

Oy	6	AspTYrLeuAlaasnAlaSerAspPheProaspTYrAlaalaAlaphGlyAsnCysThr	25
Db	353	GACTCGCACCGCTTCCACAGATGACTCACTGAATTGGATTTCACAGACTCTTCTGTAA	412
Oy	26	AspGLuaSnle---ProLeuLysMetHisTYrLeuProValileTYrGlyllelPhe	44
Db	413	AAAATAATATGTCAGGACAGTTGCCAACCATTTCTCCACCCTGTAAGCTTGCTGTC	472
Oy	45	LeuValGlyPheProGlyAsnAlaValalleSerThryrLlePheLysMetArgPro	64
Db	473	ATTGTGGCACCTTGGGGACAGCGCTGTCATCTTGTCTGTATTCACAAGAGTG	532
Oy	65	TrypLysSerSerThrillelMetLeuAsnLeuAlacysThrAspLeuLeuThyrLeu	84
Db	533	AAGACCATGACTGACATGTTCTCTTTGAATTAGCATGCTGATGCTGCTTTCCTGCC	592
Oy	85	SerLeuProPheLeulleHisTYrTrpLaseArgLysGlusAnrTYrPheGlyAspPhe	104
Db	593	ACTCTTCCCTCTGGGCC-----ATTGCTCTGCTGTCATAGGATGCTTCACACCTTC	646
Oy	105	MetcysLysPheilleArgPheSerPheHisPheAsnLeuTyrsSerSerlleLeuPheLeu	124
Db	647	ATGTGCAAGGTGTGGAACAGCATGTACAGATGAACTTCTACACTGTGTCTTCATC	706
Oy	125	ThrCysPheSerlliePheArgTYrCysValillelleHisPrometSerCysPheSerlle	144
Db	707	ATGTGCATCACTGTGGACATGACATTCAGCTTCATTCACAGGCCATGAAGCTCAGGTTGG	766
Oy	145	HisLysThrArgCys-----AlaValAlaAlaCysAlaValallellelleSerLeu	162
Db	767	AGGCAGAAAGAAGTCGTATACAGCAAGATGTGTCGATTCACATCTGGGTGATGGACGT	826
Oy	163	ValAlaValallePrometThrPheullelThrSerThrAsnArgThrAsnArgSera	182
Db	827	GTGTCTGCACCCCCAGAAATCTGTACAGTCAAGCTAGGTGGGAATGTGATATGCCACA	886
Oy	183	CysLeuAspLeuThrSerSerAspGluLeuAsnThrilleLysTrpTYrAsnLeulleu	202
Db	887	TGTACCATGTCCTACCCCTAAGGATTAAGAAATGCCAAGCTAAAGTAGAGCTGTATATCTG	946
Oy	203	ThrAlaThrThr----PheCysLeuProLeuValilleValThrLeuCysTYrThrlle	221
Db	947	AAGGTCACTGGGGGTTTTCTCCCTCTTAATGTGATGAGCGCTTCTGTATACATATC	1006
Oy	222	LleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArgArg	241
Db	1007	ATTCAATCACTTG-----GTACAGGCCCAAAGAATCATCAAGCAACAAGGCCCTGAAG	1057
Oy	242	LeuThrilleLeuLeuLeuAlaPheThyValLysPheLeuProPheHislleLeuArg	261

Df	1058	GTGACCAATCAGTCAGTCTCATGCTCTTCAATTAATGCTCAGTTCCGCCCTACACATCACTATTCTT	1117
OY	262	VallIEatg---IIeGISeRrArgLeuISerIIEser---CySerIlleIGuaSnIn	279
Df	1118	GTAGGACGGCGGTGTGAGCGCTTATGCAGTGTCATCTCCACTGACATATTCACCAAT	1177
OY	280	IleHtSGlualATyrlleValSerArgProleuAlaIalLeuAsnThPheGLySndeu	299
Df	1178	ATTGACANCTGCTTCAGGTACTGACACTATGCACTTCCTCCACAGTTGCTGTGAACCA	1233
OY	300	LeuTeuValIalValSerASpnAneheGlnalAlaLysSerThValArgCys	319
Df	1238	GTTCTCTATGTGTTTTGTTGGGAGAGANTCCGAAGAGATCTGCTGAACACCCTG-----	1291
OY	320	LysValSerGLySndeuGlnAlaLysIlySIesTyrrSer	334
Df	1292	AAGAACCTGGAGTGCATTAGCCAGCCAGAGGGGTTTCATTTCACA	1336
RESULT 7			
LOCUS	BQ038875	623 bp	mRNA linear EST 01-MAY-2002
DEFINITION	pgn1c.pk010.113 normalized chicken lymphoid cDNA library Gallus		
KEYWORDS	EST.		
SOURCE	chicken.		
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;		
TITLE	Phasianinae; Gallus.		
JOURNAL	1 (bases 1 to 623)		
COMMENT	Morgan,R.W. and Burnside,J. Chicken Lymphoid Ests Unpublished (2001) On Mar 27, 2002 this sequence version replaced gi:19772415. Contact: Joan Burnside Molecular Endocrinology University of Delaware 40 Townsend Hall, Newark, DE 19717, USA Tel: 302 831-1345 Fax: 302-831-3411 Email: joan@udel.edu, www.chickest.udel.edu.		
FEATURES			
Source	location/qualifiers		
	1..623		
	/organism="Gallus gallus"		
	/db_xref="taxon:9031"		
	/clone.pgn1c.pk010.113"		
	/clone.lib="normalized chicken lymphoid cDNA library"		
	/sex="Male and Female"		
	/tissue_type="thymus, bursa, spleen, PBL, bone marrow"		
	/lab_host="E.coli EMOD10B"		
	/note="Vector: pCMVSPORT 6"		
BASE COUNT	117 a 199 c 172 g 128 t	7 others	
ORIGIN			
Alignment Scores:			
Pred. No.:	2.55e-32	Length:	623
Score:	388.00	Matches:	79
Percent Similarity:	55.94%	Conservative:	34
Best Local Similarity:	39.11%	Mismatches:	81
Query Match:	21.91%	Indels:	8
DB:	14	Gaps:	3
US-10-023-775B-2 (1-337) x BQ038875 (1-623)			
OY	1	MetansngluProleuApTYrLeuAlaAsnIalSerAspPheProaspTYrAlaIala---	19
Df	12	ATGACCGAGATCACTCTGCTGTGAACGAGACGACCCGAGCTCTGCGCGGC	71


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QY 232 AspSerCysLeuYsglnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
    ::::: ||| ::::: ||| ::::: |||
Db 600 AACCGGACGAAGAGTCGGCGCTTGTCTGCTGCGCGGCTTCGTGCATCTTCATC 659
QY 252 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer 271
    ||||| ||| ::::: ||| :::::
Db 660 GTCTGCTTGGGCCCCC-AACGCTCTCTGAT----- 691
QY 272 IleSerCysSerIleGluAsnGlnIleHisGlnAlaTyrIleValSerArgProLeuAla 291
    ::::: ||| ::::: ||| :::::
Db 692 -----GTGCATCACTTTCCTCTCCGACAGCTCTGTACCA 727
QY 292 AlaLeuAsnThrPheGlyAsnLeuLeuTyrValValValSerAspAsnPheGln 311
    ||| ||| ||| ||| |||
Db 728 GAGGACGCTACTTGTCTTACTCTCTC----- 754
QY 312 AlaValCys---SerThrValArgCys 319
    ||||| ||| ||| ||| |||
Db 755 TGCCTGTGTGACGACGTGAGCTGC 781

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RESULT 9
LOCUS BC013202 2020 bp mRNA linear HTC 29-AUG-2001
DEFINITION Homo sapiens, clone IMAGE:4214482, mRNA.
ACCESSION BC013202.1 GI:15342000
VERSION BC013202.1 GI:15342000
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2020)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

```

```

REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: gcgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalobosbcm.tmc.edu.
Villalobos, D.K., Luna, R.A., Hale, S.M., Bullyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://Image.lnl.gov>
 Series: IRAX Plate: 26 Row: h Column: 23
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2695873
 This clone has the following problem: frame shifted.

FEATURES

source

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1..2020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4214482"
/tissue-type="Brain, anaplastic oligodendroglioma with
1p/19q loss"
/clone_id="NCI_CGAP_Brn67"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
BASE COUNT 410 a 689 c 508 g 413 t
ORIGIN

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Alignment Scores:
Pred. No.: 1,35e-29 Length: 2020
Score: 370.50 Matches: 91
Percent Similarity: 51.15% Conservative: 65
Best Local Similarity: 29.84% Mismatches: 136
Query Match: 20,92% Indels: 14
DB: 11 Gaps: 6

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US-10-023-775B-2 (1-337) x BC013202 (1-2020)

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QY 16 AspTyrAlaAlaPheGlyAsnGlyThrAspGlnIleProLeuYsMetHisTyr 35
    ::::: ||| ::::: ||| ::::: |||
Db 143 AACTTCTCCCTGGCCGACGACGACCAATGTGGCCAGACGCCACTGGAAACATCTG 202
QY 36 LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle 55
    ||| ::::: ||| ::::: ||| :::::
Db 203 TTGGCCCTTCCTACCTCTTGATTTATCTGCTTGTAGTGGCAATACCTGGCTG 262
QY 56 SerThrTyrIlePheLysMetArgProTyrLysSerSerThr-----IleIleMet 72
    ::||| ||| ||| ||| |||
Db 263 TGGCTTTTCATC-----CGAGACCAACAGTCCGGACCCGGCCAAAGTGTCTG 313
QY 73 LeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSerLeuProPheLeuHisTyr 92
    ::::: ||||| ||||| ||||| |||||
Db 314 ATGCATCTGGCGCTGGCCGACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
QY 93 TyrAlaSerGlyGluAsnTyrIlePheGlyAspPheMetCysLysPheIleArgPheSer 112
    ::| ||||| ||||| ||||| |||||
Db 374 CACTTCTCGGAACACACTGGCCATTTGGGGAATGCCATGCCGCTCACCGCTTCTC 433
QY 113 PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
    |||::: |||::: |||::: |||::: |||:::
Db 434 TTCCTACCTCAACAGTACGCGACGACTCTCTCTCTCCACGTCACACGCGACCTTC 493
QY 133 CysValIleIleHisProMetSerCysPheSerIleHisTyrThrArgCysAlaValIle 152
    |||::: |||::: |||::: |||::: |||:::
Db 494 CTGGCCATTGTGACCCCGGTCAGTCCCTTAAGCTCGGACGCCCTCTACGACACTG 553
QY 153 AlacysAlaValValTyrIleIleSerLeuValAlaValIleProMetThrPheLeuIle 172
    ||||| ||| ::::: ||| ::::: ||| :::::
Db 554 GCGTGTCTCTCTGCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 609
QY 173 ThrSerThrAsnArgThrAsnArgSer---AlacysLeuAsnLeuThrSerSerPglu 191
    ||| ::::: ||| ::::: ||| :::::
Db 610 CCACAGACCTCGGACGACCAACACACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 669
QY 192 LeuAsnThrIleLysTyrPheAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeu 211
    ::::: |||::: |||::: |||::: |||:::
Db 670 TCCAC-----CATGCCCTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
QY 212 ValIleValThrLeuCysTyrThrThrIleIleHisThrLeuThrHisGlyLeuGlnThr 231
    ::| ||||| ||||| ||||| |||||
Db 718 ATCACCACGGGTACACTCTACCTGCTGATCATCGGACCTGGGGGACGCGCGGTG 777
QY 232 AspSerCysLeuYsglnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
    ::::: ||||| ||||| ||||| |||||
Db 778 GAGAAAGCGCTCAAGACCAAGCAAGTGCATGATCCCAATGCGCGGCAATCTCTG 837
QY 252 ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGluSerArgLeuLeu 270
    ||||| |||::: |||::: |||::: |||:::
Db 838 GTCTGCTTGTGGCTTACCACTGACCGTACCGTCTGCTGCTGCTGCTGCTGCTGCTG 897
QY 271 SerIleSerCysSerIleGluAsnGlnIleHisGlnAlaTyrIleValSerArgProLeu 290
    ||||| ::::: ||| ::::: ||| :::::
Db 898 GGGGCGCTCGTGGCCGACCCGACCAATCTGCGCTGGCAAAACGACATCACTCTGCTC 957
QY 291 AlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrValValValSerAspAsnPheGln 310
    ::||| ||| ::::: ||| ::::: ||| :::::
Db 958 ACCAGCCTCAACGGGCGACCTGACCCCATCATGATATTTCTTGTGTGTGAGAGTTCGG 1017
QY 311 GlnAlaValCysSer 315
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Db 1018 CACGCGCTGTGCAC 1032

```


RESULT 10
 AU091121 971 bp mRNA linear EST 23-JAN-2001
 LOCUS AU091121
 DEFINITION lambda ZAPR-Con A stimulated leukocytes Paralicthys olivaceus cDNA clone JFCONA882F forward similar to Gallus gallus chemokine receptor-like protein (2412323A), mRNA sequence.
 ACCESSION AU091121
 VERSION AU091121.1 GI:12391161
 KEYWORDS EST
 SOURCE bastard halibut.
 ORGANISM Paralicthys olivaceus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectidae; Paralicthyidae; Paralicthys.
 REFERENCE 1 (bases 1 to 971)
 Nam, B., Hirono, I. and Aoki, T.
 Identification of expressed genes from Japanese flounder (Paralicthys olivaceus) leukocytes stimulated with Con A/PMA
 JOURNAL Unpublished (2000)
 COMMENT Contact: Ikuro Hirono
 Laboratory of Genetics and Biochemistry
 Tokyo University of Fisheries
 Konan 4-5-7, Minato-ku, Tokyo 108, Japan
 Email: hirono@tokyo-u-fish.ac.jp.
 FEATURES
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 1. 971
 /organism="Paralicthys olivaceus"
 /db_xref="taxon:8255"
 /clone="JFCONA882F"
 /clone_1lb="lambda ZAPR-Con A stimulated leukocytes"
 /cell_type="leukocytes"
 /dev_stage="adult"
 /note="common name: Japanese flounder ; injected with peptidoglycan"
 BASE COUNT 205 a 248 c 221 g 297 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,91e-30 Length: 971
 Score: 370.00 Matches: 96
 Percent Similarity: 47.66% Conservative: 57
 Best Local Similarity: 29.91% Mismatches: 140
 Query Match: 20.89% Indels: 28
 DB: Gaps: 8
 US-10-023-775b-2 (1-337) x AU091121 (1-971)
 QY 4 ProleuaspTYR-----LeualaasnaAlaSerAsp 13
 DB 21 CCGACAGACTACGAGAAATGAGAAATGACACAGACTATGACAAACAGAGCTCCGAC 80
 QY 14 PheProaspTYRAlaAlaAlaPheGlyAsnGlyThrAspGlnunleProleuLYs--- 32
 DB 81 CTCACAGCTCATATC-----TGTGAGAAAGAAAGAGAGCCCTCCGACACC 125
 QY 33 -----MethisTYRleuProValIleTYRgLYIlelePheleuValGlyPheProGly 50
 DB 126 CTCGGCACTGTTCACAGCTGTGTGTACAGCTGATCTTCCTGGTGGGTGGGTGGG 185
 QY 51 AsnAlaValAlaIleSerThrTYRlePheGlyMetArgProTrpIysSerSerThrIle 70
 DB 186 AACGGCGTATGATACAGCTCCCTGAGAGCTGGCTCTCTCCGACACTGAGATATA 245
 QY 71 IleMetIeuAsnleuAlaCysThrAspLeuTYRleuThrSerleuProPheleuIle 90
 DB 246 TACCTACTTACCTCGCCCTGGCTGACCTCATCTCTTTAACTTCCTTCGATGATG 305
 QY 91 HisTYRAlaSerGlyIleuAsnTrpIlePheGlyAspPheMetCysIysPheIleArg 110
 DB 306 GTCGACTTCTCGCTGGT-----TGGTGTGGGATTTCTCTCAAGCTGATGGC 359

QY 111 PheSerPheHisPheAsnleuTYRSerSerIleleuPheleuThrCysPheSerIlePhe 130
 DB 360 CTGATGAACATCTCAATTCCTCTGTGGAGTTTCTTTAGCTTCATGGGTTGAT 419
 QY 131 ArgTYRCysValIleIleHisPrometSerCysPheSerIleHisIleThrArgCysAla 150
 DB 420 CGGATATTGGCTATCGTTCATGCCATCCAGCATGCCAATGCGCTCCGAGAGCAGTG 479
 QY 151 ValValAlaCysAlaValAlaTrpIleIleSerleuValAlaValIlePro---MetThr 169
 DB 480 CATGTACTTGCATTTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539
 QY 170 PheleuIleThrSerThrAsnArgThrAspArgSerAlaCysleuAspLeuThrSerSer 189
 DB 540 TTTCTTTCTGTGAGAGAGGAACTAACATCCAGCTCATCTCTCTATCATCAT 599
 QY 190 AspGlnleuAsnThrIleIleSTPTyr-----AsnleuIleleuThrAlaThrPhe 207
 DB 600 CATGACATTCATGACACAACTGGTTTGTGACCAACAGACTTCGATCATATTCCTTT 659
 QY 208 CysleuProleuValIleValThrleuCysTYRThrIleIleHisIleThrHis 227
 DB 660 TTCGTACTCTGTGCTCATGAGCTACTGCTACACAGAGTGTAGTTACTTGTGTGACAC 719
 QY 228 GlyleuGlnThrAspSerCysleuGlyGlnAlaArgArgleuThrIleleuLeu 247
 DB 720 AGTCAGAAAGCCCAACA-----AACCAAGAGCCATGGAGCTGCTTACTTGTCAAT 773
 QY 248 LeuAlaPheTYRValCysPheleuProPheHisIleleuArgValIleArgIleGluSer 267
 DB 774 CTGTCTTTTGGCTCTGT 833
 QY 268 ArgleuLeuSerIle-----SerCysSerIleGlnunleHisIleGluAlaTYR 284
 DB 834 GACCTGGAGGCTCATCCATGAAGAGTGTCAAACTTTGCCCTGCGAGGCCCTC 893
 QY 285 IleValSerArgProleuAlaAlaLeuAsnThrPheGlyAsnleuLeuTYRValVal 304
 DB 894 GATGTGTCCCTGAGTCTGGAGTCTTACATGTTGCTGACCAACCTCTTATGCTTC 953
 QY 305 Val 305
 DB 954 ATT 956
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 LOCUS AL551903
 DEFINITION prime, mRNA sequence.
 ACCESSION AL551903
 VERSION AL551903.1 GI:12890291
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 946)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope, Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, web : www.genoscope.cns.fr.
 FEATURES
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 1. 946
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1060YJ18"
 /clone_1lb="LTI_NFL006.PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com

BASE COUNT 269 a 231 c 168 g 275 t 3 others

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
8	89e-30	367.50	49.64%	28.42%	946	79	59	123	17	5

US-10-023-775b-2 (1-337) x AL551903 (1-946)

```

Qy 4 ProleuaspTyrrleuAlaAsnAlaSerAspPhe---ProaspTyrrAlaAlaAlaPheGly 22
Db 55 CCATATGAT---ATACAAATGGCAACAATTACTCCGCCCTCTGCACTCCACAGGA 111
Qy 23 AsnCysThrAspGluAsnIleProleuLysMetHisTyr-----Leu 36
Db 112 AATGACTGTGAC-----CTCTATGACATACACAGCAGCCAGATAGTATG 159
Qy 37 ProValIleTyrrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSer 56
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Db 220 GTCATGTTGTAAGAAAGGAAAGAAATCACTACACCCCTCTATCAACAATTTGTC 279
Qy 77 CysThrAspLeuLeuTyrrIlePheLeuValGlyPheProGlyAsnAlaValIleSer 96
Db 280 AATTCGATATATCTTTTACACCGCTTCTCTACACGAAATAGCCTACTATGCAATGGC 339
Qy 97 GluAsnTyrrIlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsn 116
Db 340 TTGGACTGGAGAAATCGGAGATGCTTGTGTAGGATTAACGCGCTAGTGTTTTACATCAAC 399
Qy 117 LeuTyrrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrrCysValIleIle 136
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Qy 137 HisProMetSerCysPheSerIleHisLysThrArgCysAlaValAlaCysAlaVal 156
Db 460 CACCCTCTACGTCACAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 519
Qy 157 ValTyrrIleIleSerLeuValAlaValIlePromethrPheLeuIleThrSerThrAsn 176
Db 520 GTCTGGATTTCTATATTTGCTCAGACATCCCACTCTCTATCAACCTATGCAAGACAG 579
Qy 177 ArgThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys 196
Db 580 GAGCGTGAAGATTTACATCATGAGATATCCCAACTTGAAGAAATAATATCTCTCC 639
Qy 197 TrpTyrrAsnLeuIleLeuThrAlaThrPheCysLeuProLeuValIleValThrLeu 216
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AL532537
LOCUS
DEFINITION
ACCESSION
AL532537
KEYWORDS
SOURCE
ORGANISM
human.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
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source
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/clone="CS0DM006YC06"
/clone_1tb="LTI_NFL001_NBC4"
/sex="male"
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/lab_host="DH10B"
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http://fulllength.invitrogen.com"
BASE COUNT 260 a 220 c 160 g 264 t
ORIGIN
Alignment Scores:
Pred. No.: 1.07e-29
Score: 366.50
Percent Similarity: 50.00%
Best Local Similarity: 29.10%
Query Match: 20.69%
Length: 904
Matches: 78
Conservative: 56
Mismatches: 117
Indels: 17
Gaps: 5
US-10-023-775b-2 (1-337) x AL532537 (1-904)
Qy 4 ProleuaspTyrrleuAlaAsnAlaSerAspPhe---ProaspTyrrAlaAlaAlaPheGly 22
Db 74 CCATATGAT---ATACAAATGGCAACAATTACTCCGCCCTCTGCACTCCACAGGA 130
Qy 23 AsnCysThrAspGluAsnIleProleuLysMetHisTyr-----Leu 36
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Qy 37 ProValIleTyrrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSer 56
Db 179 CCTCTGATTAACAGCTGCTTCATCATTTGGGCTGCTGGAACTTACTAGCCTTGTC 238
Qy 57 ThrTyrrIlePheLysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAla 76
Db 239 GTCATTTGTTAAGAAAGGAAAGAAATCACTACACCCCTCTATTCACAAATTTGTC 298
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Db      299 ATTTCTGATATCTTTTACACACCGCTTGCCTACACGAATAGCCCTACTATCAATGAGGC 358
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      359 TTTGACTGAGAGATGAGATGCTGTGTAGATCAATGCTGCTACTGTTTATCAATCAAC 418
      117 LeuYrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIle 136
      419 ACATATGACAGCTGTGACTTATAGACTCCCTGAGATGATGACCGCTTCAATGCTGTG 478
      137 HisPrometSerCysPheSerIleHisLysTrpArgCysAlaValAlaIaCysAlaVal 156
      479 CACCTCTACGCTACAAACAAGATMAAAGATTGAACAGCAAAAGCGCTGTCATATTT 538
      157 ValTrpIleIleSerLeuValAlaValIlePrometThrPheLeuIleHisSerThrAsn 176
      539 GTCTGATTTCTAGTATTTGCTCAGACACCTCCATCCTTCATCAACCTTATGTCAAAGCAG 598
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      197 TrpTyrAsnLeuIleLeuThrAlaThrTrpPheCysLeuProLeuValIleValThrLeu 216
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      217 CysTyrThrThrIleIleHisThrLeu-----ThHisLysLeuGlnThr 231
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LOCUS      AL547762 LRI_NFL006.PL2 Homo sapiens cDNA clone CSOD1017YN05 5
DEFINITION      prime, mRNA sequence.
ACCESSION      AL547762
VERSION      AL547762.1 GI:12882129
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
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            Eumetazoa; Euthera; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 931)
            L1,W.B., Gruber,C., Jesse,J. and Polayes,D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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            vector. Library was normalized. Library was constructed by
            Life Technologies. Contact : Feng Liang Life Technologies,
            a division of invitrogen 9800 Medical Center Drive

```

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : filangeli@life.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 268 a 224 c 165 g 273 t 1 others

ALIGNMENT Scores:

Pred. No.:	Length:	931
Score:	366.50	78
Percent Similarity:	50.008	Conservative: 56
Best Local Similarity:	29.108	Mismatches: 117
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US-10-023-775b-2. (1-337) x AL547762 (1-931)

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      106 AATGACTGTGAC-----CTTATGACATCAGACAGCAGCGCCAGATAGTAAG 153
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      57 ThrTyrIlePheLysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAla 76
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      334 TTTGACTGAGAGATGCGAGATGCTGTGTAGATCAATGCGCTGATGTTTATCAATCAAC 393
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      394 ACATATGACAGCTGTGACTTATGACCTGCTGAGATGATGACCGCTTCAATGCTGTG 453
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IMAGE:5383884 5', mRNA sequence.
ACCESSION BQ396255
VERSION BQ396255.1 GI:21083932
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
Xenopodinae; Silurana.
1 (bases 1 to 641)
NIH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml.
National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apds-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: L1AM1977 row: N column: 13
Seq primer: M13RPI reverse primer (ABI).
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Query Match: 19.93% Indels: 2
DB: 14 Gaps: 1
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OY 46 ValGlyPheProGlysnAlaValIleSerThyTyrIlePheMethArgProTyr 65
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OY 66 LysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeuTyrLeuThrSer 85
DB 229 AACGCTTCACCAACCTACATGTTCAACCTGGCCATTCGCAACATGATGTCGATCTCC 288
OY 86 LeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIlePheGlyAspPheMet 105
DB 289 CTCGCCCTGCTGCTATTACTACTGCAAGGGGAGCAACATGCGCGTTCGGCGTGGCTTG 348
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DB 409 TGCATGACGATCCACCGCTTCCTCGGAGATCGTCAACCAATGAATACATCGGTGCTG 468
OY 146 LysThrArgCysAlaValAlaAlaCysAlaValAlaValIleIleSerLeuAlaVal 165
DB 469 AAGCTCGCGAATGCTCGAATATTTCCGTGCTCTGGGGTATTCGCTTCGCCCTGTCAG 528
OY 166 IleProMetThrPheLeuIleIleSerThrAsnArgThrAsnArgSerAlaCysLeuAsp 185
DB 529 TCCCTATATTTGATCTTGTATTACCAACGATTCATGGGACACACACCTGCTGATAC 588
OY 186 LeuThrSerSerAspGluAsnTyrIleLysTyrTyrAsnLeuIle 201
DB 589 ACTTCACGCGATGATCTATTGACAACTTGTGTGTACAGACAGATGTC 636
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DEFINITION AL675845 XGC-gastrula Silurana tropicalis cDNA clone Tgas051n19 5',
mRNA sequence.
ACCESSION AL675845
VERSION AL675845.1 GI:19532219
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
Xenopodinae; Silurana.
1 (bases 1 to 638)
Taylor, R., Ashurst, J.L., Cronling, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
JOURNAL COMMENT Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: Tgas051n19.plcSP6
Sequencing primer: PlcSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
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into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT 134 a 180 c 144 g 179 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2.47e-28 Length: 638
Score: 352.00 Matches: 66
Percent Similarity: 59.66% Conservative: 39
Best Local Similarity: 37.50% Mismatches: 69
Query Match: 19.88% Indels: 2
DB: 9 Gaps: 1
US-10-023-775b-2 (1-337) x AL675845 (1-638)
OY 26 AspGluasnIleProLeuMethIstYrLeuProValIleTygIleIlePheLeu 45
DB 111 GACGAGAGAT-----TTCAAGTAGCTGCTCCCGTCCGTCGACGACGATGTCCTGC 164

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model.

Run on: May 29, 2003, 23:41:35 ; Search time 62 Seconds

(without alignments)
1666.937 Million cell updates/sec

Title: US-10-023-775B-2

Perfect score: 1771

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Ygapop 10.0 , Ygapext 0.5	
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Delop 6.0 , Delext 7.0	

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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8	400	22.6	984	3	US-08-513-974B-57
9	400	22.6	1023	3	US-08-513-974B-379
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11	394.5	22.3	1901	1	US-08-153-848-43
12	394.5	22.3	1901	3	US-09-299-843A-43

13	394.5	22.3	1901	4	US-09-088-337B-43	Sequence 43, Appl
14	394.5	22.3	1901	5	PCR-US93-11153-43	Sequence 43, Appl
15	394.5	22.3	2453	5	PCR-US95-07180-1	Sequence 1, Appl1
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18	388.5	21.9	1764	3	US-08-767-993-12	Sequence 12, Appl
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20	388.5	21.9	2732	1	US-08-472-840-60	Sequence 60, Appl
21	388.5	21.9	2732	2	US-08-476-976-60	Sequence 60, Appl
22	388.5	21.9	2732	3	US-08-474-410-60	Sequence 60, Appl
23	388.5	21.9	2732	4	US-08-486-673B-60	Sequence 60, Appl
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25	388.5	21.9	3480	1	US-07-789-184-219	Sequence 219, App
26	388.5	21.9	3480	1	US-08-475-263-219	Sequence 219, App
27	388.5	21.9	3480	1	US-08-485-886-219	Sequence 219, App
28	388.5	21.9	3480	2	US-08-477-362-219	Sequence 219, App
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44	376.5	21.3	1255	1	US-08-472-840-3	Sequence 3, Appl1
45	376.5	21.3	1255	2	US-08-476-976-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-559-524A-1
; Sequence 1, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1996 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 625..1626
US-08-559-524A-1

Alignment Scores:
Pred. No.: 3.8e-38
Score: 467.00
Percent Similarity: 55.23%
Best Local Similarity: 35.29%
Query Match: 26.37%
                Length: 1996
                Matches: 108
                Conserved: 61
                Mismatches: 125
                Indels: 12
                Gaps: 6

US-10-023-775B-2 (1-337) x US-08-559-524A-1 (1-1996)
QY 23 AsnCysThrAspGluAsn-----IleProLeuLysMetHisTyrLeuPro 37
Db 646 AATGCAACTGCAAAAACCTGGCTGGCAGACAGCGCTCCCTGGAAGAGTACTACTTCC 705
QY 38 ValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThr 57
b 706 ATTTTATGAGATGAGTTCGTTGTCGAGCTCCTTGAATACCATGTTGTTTACGGC 765
QY 58 TyrIlePheLysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCys 77
Db 766 TACATCTTCTCTGAGAACTGGAACAGCAGTAAATTTATCTCTTAACCTCTCTC 825
QY 78 ThrAspLeuLeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGlu 97
Db 826 TCTGACTTACCTTTCCTGTCACCCCTCCATGCTGAAGAGATTATGCCAATGGA--- 882
QY 98 AsnTyrIlePheGlyAspMetCysLysPheIleArgPheSerPheHisPheAsnLeu 117
Db 883 AACTGGATATATGAGAGCGTCTGTCATTAACCAACCGATATGCTTCATGCCAACCCTC 942
QY 118 TyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHis 137
Db 943 TATACAGCATCTCTCTTTCACCTTTATACAGATATGATCTGATTAATTAAGTAT 1002
QY 138 PrometSerCysPheSerIleHisLysThrArgCysAlaValAlaIaCysAlaValAla 157
Db 1003 CCTTTCGAGACACCTTTCGCAAAAGAAAGAGATTGCTATTAACTCTTGCCAT 1062
QY 158 TyrIleIleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArg 177
Db 1063 TGGGTTTATGTAACCTTATAGATTAACCAATACCTCCCTTATTAATCTGTTATACT 1122
QY 178 ThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspLysLeuAsnThrIleLysTyr 197
Db 1123 GACAATGGCAGCACACCTGTATGATTGCAAGTTCTGCAAGCCCACTCAACCTCAT 1182
QY 198 TyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCys 217
Db 1183 TACAGCATGCTGTAAACACTGTGGGGTCTCTTATTCCTTTTGGAGATGTTTCTT 1242
QY 218 TyrThrThrIle---IleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLys 236
Db 1243 TATTACAAAGATTGCTCTCTCTTCAACAGCAAGAGATAGGAGGTTGCTACTGCTCTCCC 1302
QY 237 ---GlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeu 255
Db 1303 CTGGAAGGCTCTCAACCTTGGTCATCATGAGGAGTGTATCTTCTGTGCTTTTACA 1362
QY 256 ProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer-----Ile 272
Db 1363 CCTATACACCTCATGCGAATGTAGAGATCGCTTACAGCCTTGAGAGATTGGAAGCAGTAT 1422
QY 273 SerCysSerIleGluLysGlnIleHisGluAlaTyrIleValIleValIleValIleVal 292
Db 1423 CAGTGCACCT---CAGGTCGATCATCACTCTTTTACATTTGACACGGGCTTTGGGCTTT 1479

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QY 293 LeuAsnThrPheGlyAsnLeuLeuLeuTyrValValSerAspAsnPheGlnAla 312
Db 1480 CTGAACAGTGCATCAACCCGCTCTCTATTTCTTTGGAGATCACTTACGAGCATG 1539
QY 313 ValCysSerThrValArg 318
Db 1540 CTGATGAATCACTGAGA 1557

RESULT 2
US-08-749-707-1
: Sequence 1, Application US/08749707
: Patent No. 6063582
: GENERAL INFORMATION:
: APPLICANT: Conley, Pamela B.
: APPLICANT: Jantzen, Hans-Michael
: TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
: STREET: 1800 M Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036-5869
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/749,707
: FILING DATE: 15-NOV-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Adler, Reid G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 044481-5010-01-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-467-7000
: TELEFAX: 202-467-7176
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1996 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 625..1626
: US-08-749-707-1

Alignment Scores:
Pred. No.: 3.8e-38
Score: 467.00
Percent Similarity: 55.23%
Best Local Similarity: 35.29%
Query Match: 26.37%
                Length: 1996
                Matches: 108
                Conserved: 61
                Mismatches: 125
                Indels: 12
                Gaps: 6

US-10-023-775B-2 (1-337) x US-08-749-707-1 (1-1996)
QY 23 AsnCysThrAspGluAsn-----IleProLeuLysMetHisTyrLeuPro 37
Db 646 AATGCAACTGCAAAAACCTGGCTGGCAGACAGCGCTCCCTGGAAGAGTACTACTTCC 705
QY 38 ValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThr 57
Db 706 ATTTTATGAGATGAGTTCGTTGTCGAGCTCCTTGAATACCATGTTGTTTACGGC 765
QY 58 TyrIlePheLysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCys 77

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Db 766 TACATCTCTCTGAGAACTGGAACAGACAGTAATATTTATCTTTAACTCTCTGTC 825
Qy 78 ThrAspLeuLeuThyrLeuThrSerLeuProPheLeuIleHisThyTyrAlaSerGlyGlu 97
Db 826 TCTGACTTACGCTTTCTTGCGACCCCTCCCATCGATGATAGAGAGTTATCCCATGA--- 882
Qy 98 AsnTrpIlePheGlyAspPheMetCysIlyPheIleArgPheSerPheHisPheAsnLeu 117
Db 883 AACTGATATATGAGACAGCTGCTGTCATTAAGCAACCGATATGCTTATGTCACCACTTC 942
Qy 118 TyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHis 137
Db 943 TATACCAACATCTCTTCTTCTTCTTATACACATAGATACGACTGATATTAAGTAT 1002
Qy 138 PrometSerCysPheSerIleHisIlyThrArgCysAlaValAlaIleCysAlaValAla 157
Db 1003 CTTTCCGAGAACACCTTCTGCAAAAGAAAGATTGCTATTATTAATCTCTGCGCAT 1062
Qy 158 TrpIleIleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArg 177
Db 1063 TGGGTTTATAGTAACCTTATAGTACTACCATACACTCCCTTATATAATCTGTATAACT 1122
Qy 178 ThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleIlyStrp 197
Db 1123 GACAAATGGCACCACTGTATGATTTTTCAGAGTCTCGAGACCCCACTACAACCTCAT 1182
Qy 198 TyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleValIleThrLeu 217
Db 1183 TACACATGTCCTTAACACTGTGGGGTTCCTTAATCTCTTGTGATGCTGTTCTTT 1242
Qy 218 TyrThrThrIle---IleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeu 236
Db 1243 TATTACAGATGCTCTCTCTCTTAAGCAGAGAAAGAGAGCTTCTACTGCTGCCCC 1302
Qy 237 ---GlnIlyAlaArgArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeu 255
Db 1303 CTTGAAGAGCCCTCAACTGTGTCATCATGACAGATGATCTCTCTCTCTCTTTTACA 1362
Qy 256 ProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer-----Ile 272
Db 1363 CCGTATCACGTCATGCGGAGATGAGAGATCGCTTCAACGCTGGGGGCTGGAGCAGTAT 1422
Qy 273 SerCysSerIleGluAsnGlnIleHisGlnAlaTyrIleValSerArgProLeuAlaIle 292
Db 1423 CAGTGCACT---CAGGTGCTGATCAACCTTTTACATGTGACAGCGGCTTTGGCTTT 1479
Qy 293 LeuAsnThrPheGlyAsnLeuLeuLeuThyrValValValSerAspAsnPhenGlnGlnAla 312
Db 1480 CTGAACAGTGCATGACCCCTGCTCTTCTTCTTTTGGAGATCATTCACTTCAAGGACATG 1539
Qy 313 ValCysSerThrValArg 318
Db 1540 CTGATGATCACTAGTGA 1557

RESULT 3
US-08-442-134A-1
; Sequence 1, Application US/08442134A
; Patent No. 5556088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009

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; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ. ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-442-134A-1

Alignment Scores:
Score: 3.04e-35 Length: 1842
Percent Similarity: 438.00 Matches: 93
Best Local Similarity: 53.908 Conservative: 59
Query Match: 32.988 Mismatches: 118
DB: 24.738 Indels: 12
Gaps: 4

US-10-023-775b-2 (1-337) x US-08-442-134A-1 (1-1842)
Qy 28 AsnIleProLeuIlyMetHisIlyThrLeuProValIleTyrGlyIleIlePheLeuValGly 47
Db 138 AACGAGACTTCAAGTACAGTGCCTGCTGCTGCTTCTTACAGCGGTGCTGCTGGG 197
Qy 48 PheProGlyAsnAlaValAlaValIleSerThrTyrIlePheIlyMetArgProTrpIlySer 67
Db 198 CTGTGCTGACAGCGGCTGCGCTCTTCAATCTTCTTGTGCGGCTCAAGACCTGAGTGG 257
Qy 68 SerThrIleIleMetLeuAsnLeuAlaCysThrAspLeuLeuThrSerLeuPro 87
Db 258 TCCACCAATATATATGTTCCACCTGCTGTGTGATGACAGCATATGCGGCTCCCGCG 317
Qy 88 PheLeuIleHisIlyTyrAlaSerGlyIlyAsnTrpIlePheGlyAspPheMetCysIly 107
Db 318 CTGCTGCTTATTTACTACGCGCGCGCGGACACACTGCGCTTACAGCAGGCTCTTCAAG 377
Qy 108 PheIleArgPheSerPheHisPheAsnLeuThyrSerSerIleLeuPheLeuThrCysPhe 127
Db 378 CTGCTGCGCTTCTCTTCAACCAACCTTACTGACAGATCCTCTTCTCACTGACATC 437
Qy 128 SerIlePheArgTyrCysValIleIleHisIlyPrometSerCysPheSerIleHisIlyThr 147
Db 438 ACGGTGACACCGGTGCTGCGCTTACACCTGCTGCGCTGCGCTGCGGCGCGGCG 497
Qy 148 ArgCysAlaValAlaValAlaCysAlaValAlaValIleSerLeuValAlaValIlePro 167
Db 498 CCGTACGCTGCGCGGCTGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 557
Qy 168 MetThrPheLeuIleThrSerThrAsnArgThrAsnArgSerAlaCysLeuAspLeuThr 187
Db 558 GTGCTCTACTTTGTACACACAGCGGCGGC---GGCGCGCTAACCTGCGCACGACACCTG 614

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Db      906 AACATGCGCTACAGATTACCGG---CTGGCGAAGTCTAACAGTTGCTTGAACCCGTG 962
Qy      301 LeuTyr 302
Db      963 CTCTAC 968

RESULT 5
US-08-446-088A-1
Sequence 1, Application US/08446088A
Patent No. 5691156
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harden, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691156th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,088A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D. Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 57..1181
US-08-446-088A-1

Alignment Scores:
Pred. No.: 3 04e-35 Length: 1842
Score: 438.00 Matches: 93
Percent Similarity: 53.90% Conservative: 59
Best Local Similarity: 32.98% Mismatches: 118
Query Match: 24.73% Indels: 12
Db: 1 Gaps: 4

US-10-023-775B-2 (1-337) x US-08-446-088A-1 (1-1842)
Qy      28 AsnIleProLeuValMetHisTyrIleuProValIleTyrGlyIleIlePheLeuValGly 47
Db      138 AACGAGACACTTAAGTACGTGCTGCGTGCCTGTCCTACGCGCGTGTGCTGCTGGG 197
Qy      48 PheProGlyAsnAlaValIleSerThrTyrIlePheLysMetArgProTyrPlySer 67

```

[illegible]

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1 STATE: MA
2 COUNTRY: USA
3 ZIP: 02109
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #1.0, Version #1.30
10
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/513,974B
13 FILING DATE: 14-SEP-1995
14 CLASSIFICATION: 536
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: PCT/J95/01599
17 FILING DATE: 10-AUG-1995
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: JP 7-093989
20 FILING DATE: 19-AUG-1995
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: JP 7-057186
23 FILING DATE: 16-MAR-1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: JP 7-007177
26 FILING DATE: 20-JAN-1995
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: JP 6-326611
29 FILING DATE: 28-DEC-1994
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: JP 6-270017
32 FILING DATE: 02-NOV-1994
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: JP 6-236357
35 FILING DATE: 30-SEP-1994
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: JP 6-236356
38 FILING DATE: 30-SEP-1994
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: JP 6-189274
41 FILING DATE: 11-AUG-1994
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: JP 6-189273
44 FILING DATE: 11-AUG-1945
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: JP 6-189272
47 FILING DATE: 11-AUG-1994
48 ATTORNEY/AGENT INFORMATION:
49 NAME: Resnick, David S.
50 REGISTRATION NUMBER: 34,235
51 REFERENCE/DOCKET NUMBER: 45753
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: 617-523-3400
54 TELEFAX: 617-523-6440
55 INFORMATION FOR SEQ ID NO: 41:
56 SEQUENCE CHARACTERISTICS:
57 LENGTH: 984 base pairs
58 TYPE: nucleic acid
59 STRANDEDNESS: double
60 TOPOLOGY: linear
61 MOLECULE TYPE: cDNA
62
63 US-08-513-974B-41
64
65 Alignment Scores:
66 Pred. No.: 6,61e-34 Length: 984
67 Score: 421.00 Matches: 96
68 Percent Similarity: 48.29% Conservative: 45
69 Best Local Similarity: 32.88% Mismatches: 125
70 Query Match: 23.77% Gaps: 26
71 DB: 3 Gaps: 5
72
73 US-10-023-775B-2 (1-337) x US-08-513-974B-41 (1-984)
74
75 36 LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle 555
76 ||| ::||| ::::||| ::||| ||| |||||

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Db      85  CTAACCCCGGATATACGCGGGGCGTGGTGGCGGCGTGCACCTGAACATCTGGCATTT 144
Oy      56  SerThrTyrllePheIysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeu 75
Db      145  GCCCAGATGTGCCCATCCGCGGACCCGACCCGCTGGCTGGGTGTACACCCCTGAACCTG 204
Oy      76  AlAcysThrAspLeuLeuTyrlleThrSerIleuProPheLeuIleHisTyrrTyAlaSer 95
Db      205  GCACGTGGCGGACCTGTATGTATGGCTGTGTACTACACCCCTACTATTAATATACGACGA 264
Oy      96  GtGluGlnAsnIrrPheIleGlyAspPheMetCysIlyspPheIleArgPheSerHisPhe 115
Db      265  GGGGACACACGCGCCCTTCGGAAGACCTCGCGCTCCGCCCTTGTAGAGCTTCCTTTATGCC 324
Oy      116  AsnLeuTyrrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrrValIle 135
Db      325  AACTCATATGGACGATCTCTGTCCCTACCTCATATTACTTCACAGCGCTACCTGGGACAT 384
Oy      136  IleHisProMetSerCysPheSerIleHisIlys-----ThrArgCysAlaValVal 152
Db      385  TGCACACCCCTGGCT-----TCCTGGCAACAAGCTGGAGGTGCGCGTGGCTTGGGTA 438
Oy      153  AlAcysAlaValIrrPheIleSerLeuValAlaValIleProMetThrPheLeuIle 172
Db      439  GTGTGTGGAGTCTGTGTGGCTGGCTGTGACAGCCCGACGCTGCTGCCACGACAGTCTTGCT 498
Oy      173  ThrSerThrAsnArgThrAsnArgSerAlaCysIleAspLeuThrSerSerAspGluLeu 192
Db      499  GCCACAGGCATCCAGCGGACCGGACCATGTGTCTACAGACCTGAGGCCACCATCTGTCT 558
Oy      193  AsnThrIleLysTrpPlyrAsnLeuIleLeuThrAlaThrIlePheCysLeuProLeuVal 212
Db      559  ACTGCGTACCTGCCCTATGTATGGCGCTACAGCGCTACAGGCTCTTGTGCGCTTCATATA 618
Oy      213  IleValThrLeuCysTyrrThrThrIleIleHisThrIleHisGlyLeuGlnThrAsp 232
Db      619  GCCTTACTGGCTTGTATGTGTGGCATGGCCGCCCGCTG----- 657
Oy      233  SerCys-----LeuLysGlnLysAlaArg 240
Db      658  ---TGTCGCCAGATGGCCACAGAGTCTGTGGCCCAAGAAGCGGACGAGACAGCGGCT 714
Oy      241  ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrrValCysPheLeuProPheHisIleLeu 260
Db      715  CGTATGGCTGTGGTGGTGGCAGCTGTCTTGGCATCACACTTCGCGCTTCCACATACAC 774
Oy      261  ArgValIleArgIleGluSerArgLeuLeu---SerIleSerCysSerIleGluAsnGln 279
Db      775  AAGACAGCCACTTGGCTGTGGCTTCACAGCCCGGCTGTCTCTTGGCCCTGTCTGGAAAC 834
Oy      280  IleHisGluAlaTyrrIleValSerArgProLeuAlaLeuAsnThrPheGlyAsnLeu 299
Db      835  TTGCGTGGCGCTACAAAGGACACTCGGCGCTTGCAGATGTGCACAGATGTCTGGACCC 894
Oy      300  LeuLeuTyrrValValValSerAspAsnPheGln 311
Db      895  ATTCTCTTACTTTCACACACAGAAATTCGCGGCG 930

RESULT 7
US-08-513-974B-370
; Sequence 370, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hisonoya, Shuji
; APPLICANT: Hisonoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtsuki, Tetsuya
; APPLICANT: Fukushima, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESSES:

```

ADDRESSEE: DIRK, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093969
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 370:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 28...1011
S-08-513-974B-370

```

1  APPLICANT: FUKUSUMI, SHOJI
2  APPLICANT: Onogi, Kazuhiko
3  TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN
4  TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
5  NUMBER OF SEQUENCES: 380
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: DIRK, BRONSTEIN, ROBERTS & CUSHMAN, LLP
8  STREET: 130 Water Street
9  CITY: Boston
10 STATE: MA
11 COUNTRY: USA
12 ZIP: 02109
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/513,974B
21 FILING DATE: 14-SEP-1995
22
23 CLASSIFICATION: 536
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/JP95/01599
27 FILING DATE: 10-AUG-1995
28
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: JP 7-093989
31 FILING DATE: 19-AUG-1995
32
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: JP 7-057186
35 FILING DATE: 16-MAR-1995
36
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: JP 7-007177
39 FILING DATE: 20-JAN-1995
40
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: JP 6-326611
43 FILING DATE: 28-DEC-1994
44
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: JP 6-270017
47 FILING DATE: 02-NOV-1994
48
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: JP 6-236357
51 FILING DATE: 30-SEP-1994
52
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: JP 6-236356
55 FILING DATE: 30-SEP-1994
56
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: JP 6-189274
59 FILING DATE: 11-AUG-1994
60
61 PRIOR APPLICATION DATA:
62 APPLICATION NUMBER: JP 6-189273
63 FILING DATE: 11-AUG-1995
64
65 PRIOR APPLICATION DATA:
66 APPLICATION NUMBER: JP 6-189272
67 FILING DATE: 11-AUG-1994
68
69 ATTORNEY/AGENT INFORMATION:
70 NAME: Resnick, David S.
71 REGISTRATION NUMBER: 34,235
72 REFERENCE/DOCKET NUMBER: 45753
73
74 TELECOMMUNICATION INFORMATION:
75 TELEPHONE: 617-523-3400
76 TELEFAX: 617-523-6440
77
78 INFORMATION FOR SEQ ID NO: 57:
79 SEQUENCE CHARACTERISTICS:
80 LENGTH: 984 base pairs
81 TYPE: nucleic acid
82 STRANDEDNESS: double
83 TOPOLOGY: linear
84
85 MOLECULE TYPE: CDNA
86
87 US-08-513-974B-57
88
89 Alignment Scores:
90 Pred. No.: 9,1e-32 Length: 984
91 Score: 400.00 Matches: 93

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Percent Similarity:	47.5%	Conservative:	44
Best Local Similarity:	32.2%	Mismatches:	141
Query Match:	22.5%	Indels:	10
DB:	3	Gaps:	4

US-10-023-775B-2 (1-337) x US-08-513-974B-57 (1-984)

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Conservative: 4
Mismatches: 1
Indels: 10
Gaps: 4
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QY	3	LysMeethIstyLeuLeuProValIleuArgIleIlePheLeuValIGlyPheProGlyAsn	51
Db	73	AMGCAACSTGCTGCTGCACTGTTATTCGGCGGCTGCGGCTGCGCTGCGCTGAC	1322
QY	52	AlaValIleSerThrTyrllePheLeuMetArgProTrpLysSerSerThrIleIle	71
Db	133	AMCTGTGATTAACCAAGATGACAGCTGCGCGCGCGCTGACCGGACCGGCGCGCTGTAC	192
QY	72	MetLeuAsnLeuAlaCysThrAspLeuLeuTyrlleThrSerLeuProPheIleHis	91
Db	193	ACCCATAACCTTGCTGCTGCTGCACTGCTATATGCTGCTGCTGCTGCTGCTGCTATATAC	2522
QY	92	TyrlleValSerGlyIleuAsnTrpIlePheGlyAspPheMetCysLysPheIleArgPhe	1111
Db	253	AACATAGGCCAAGGATGATCATCGGCCCTTTGGCGACTTCGGCTGCGCGCTGCTGCGCTTC	3122
QY	112	SerPheHisPheAsnLeuTyrlleSerSerIleLeuPheLeuThrCysPheSerIlePheArg	1311
Db	313	CTCTTTATAGCCAACTGCACTGCAAGGACATCTCTTCCACACTGATCAAGCTTCACAGCG	3727
QY	132	TyrlleValIleIleHisProMetSerCysPheSerIleHisLys-----ThrArg	148
Db	373	TACCTGGGATGCTGCCACCGCGCTGGCCCCCTGG-----CACMAACGGGGGGCGGCGG	4226
QY	149	CysAlaValIleAlaCysAlaValIleValTrpIleIleSerLeuValAlaValIleProMet	168
Db	427	GCCTGCGCTGCTAGTGTGTATACCTGTGGGCTGCGCGCTGACACCCAGTGCCTGCCACA	486
QY	169	ThrPheLeuIleThrSerThrAsnTrpThrAsnArgSerAlaCysIleuAspLeuThrSer	188
Db	487	GCCATCTTGCTGCTGCCAGGACATCCAGGGATACCGCACTGTCTGTATGACTTAGCGCG	546
QY	189	SerAspGluLeuAsnThrIleLysTrpTyrlleAsnLeuIleuThrAlaThrThrPheCys	208
Db	547	CCGCGCTGCGCACCAACCAATATGCGGTATGGACATGGCTCATGTCATCGGCTTCG	606
QY	209	LeuProLeuValIleValThrLeuCysTyrlleThrIleIleHisThrLeuThrHisGly	228
Db	607	CTGCTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	666
QY	229	LeuGlnThrAspSerCysLeuLysGln-----LysAlaArgLeuThrIle	244
Db	667	GATGCGCGCGGACAGACCTGTGGCCACAGAGGCGGCTGCGCAAGGCGCGCGCATGGCGCTG	726
QY	245	LeuLeuLeuLeuAlaPheTyrlleValCysPheLeuProPheHisIleLeuArgValIleArg	264
Db	727	GTGGTGCGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	786
QY	265	IleGlu---SerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIleHisGluAla	283
Db	787	CTGGCAGTGGGCTGCAGCGCGGCGCTGCCCTGCTGCTGATTTGGAGGCTTTGGACGGCGCC	846
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Db	847	TACAAAGGACACGCGCGCTTGGCCAGTGTCCAAAGCGGTGCGACCCCATCTCTCTAC	906
QY	304	ValValSerAspAsnPheGlnGln	311
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RESULT 9
US-08-513-974B-379
; Sequence 379, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji

```

APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Yetsuya
APPLICANT: Fukushima, Shoji
APPLICANT: Ohgi, Kazuhito
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ. ID NO: 379:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS

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US-08-513-974B-379	LOCATION: 37..1020
Alignment Scores:	
Pred. No.:	9,62e-32
Score:	400.00
Percent Similarity:	47.57%
Best Local Similarity:	32.29%
Query Match:	22.59%
DB:	3
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QY	52 AlAlValIleSerIyIreUValIlePheUyMeIaYpRoTprIySerSerThrIleIle 71
DB	169 ATCTGTGCTATTACCCAGATCTGCACAGTCCCGCCGCGCCCTGCAGCCCGACGGCGGTATC 228
QY	72 MetIeuAsnIeuAlaCysThrIAspIeuIeUThrIleUThrSerIeuProPheUleHis 91
DB	229 ACCCTAAACCTTCTGCTGCTGACCTGATATGCGCTGCTGCGCCCTGCTGCTATCTAC 288
QY	92 TyrTyrAlaSerGIyIuAsnTrIlePheGIyAspPheMetCysIysPheIleArgPhe 111
DB	289 AACTATGCCCAAGGTGATACGTGGCCCTTGGCCGCACTTGGCGGCTGCGCGCTGCGGCTTC 348
QY	112 SerPheHisPheAsnIeuYrSerSerIleIeuPheIeuThrCysPheSerIlePheArg 131
DB	349 CTCTCTATGCCAAGCTGCAGCGACACATCCCTTCTCTCACCCTGATCAGCTTCCAGCC 408
QY	132 TyrCysValIleIleHisPrometSerCysPheSerIleHisIlys-----ThrArg 148
DB	409 TACCTGGGCACTGCGCCACCGCGTGGCGCCCTGG-----CACAAACGTGGGGCGCGCGG 462
QY	149 CysAlaValAlaAlaCysAlaValAlaValTrIleIleSerIeuValAlaValIlePromet 166
DB	463 GCTGCGGCTAGTGTGTGTAAACGCTGTGGCGCGGTGCACACCCAGTGGCTGCCACA 522
QY	169 ThrPheIeuIleThrSerThrAsnArgThrAsnArgSerAlaCysIeuAspIeuThrSer 188
DB	523 GCATCTGCTGCTGCACAGGACGATCCAGGTAAACGCACTGCTGTATGACCTCAGCCG 582
QY	189 SerAspIeuIeuAsnThrIleUyStrIyTrpIyAsnIeuIleUThrAlaThrIlePheCys 208
DB	583 CCTGCCCTGCGCACCCCATATATGCCCTTATGGCAAGCTGCATCTGATGAGGCTCTCG 642
QY	209 IeuProIeuValIleValIleThrIeuCysYrThrTrIleIleHisIleUThrIleHisGIy 228
DB	643 CTGCGCTTTGCTGCTGCTGCTGCGCTGCTACTGTCTCTCTGCGCTGCGGCTGCGCGCAG 702
QY	229 IeuGIuThrAspSerCysIeuIySGLN-----LysAlaIArgIleUThrIle 244
DB	703 GATGGCGCGGACAGAGCTGTGGCGCCAGAGCGGCGGTGGCAAGCGCGCGCGCATGGCGGTG 762
QY	245 IeuIeuIeuIeuAlaIleIyValCysPheIeuProIleHisIleIleUArgValIleArg 264
DB	763 GTGTGTGCTGCTGCTTTCCTTGCATCAGCTTCGCGCTTTCACATCCACCAACAGAGCTTAC 822
QY	265 IIGLIU---SerArgIeuIeuSerIleSerCysSerIleGIuAsnGIuIleHisGIuAla 283
DB	823 CTGGCAGTGGGCTGCAGCGCGGGCGCCCTCCCTGCATCTATTTGGAGCGCTTGGACGGCC 882
QY	284 TyrIleValSerArgProIeuAlaIleUAsnThrPheGIyAsnIeuIeuIeuYrVal 303
DB	883 TACAAAGGACGCGCGCGCTTGTCCAGATGCCAACACGCTGTGGACCCCATCTCTCTTAC 942
QY	304 ValValSerAspAsnIleGIuIn 311
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      36 LeuProValIleIleIleIleIleIleValIleIleIleIleIleIleIleIle 55
      800 TTGGCCCTCTTACCTTCTGGATTATTCCTGCTTACCTTGGCAATACCTGGCTCTG 859
      56 SerThrTyrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 72
      860 TGGCTTTTCATC-----CGAGACCAACAGTCCGGGACCCCGGCAACGATGCTCCTG 910
      73 LeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSerLeuProIleIleIleIle 92
      911 ATGCATCTGGCCCTGGCCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 970
      93 TyrAlaSerGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 112
      971 CACTTCTCTGGAGAACCACTGCGCATTTGGGGAATGCAATGCCGCTCACCGGCTTCTC 1030
      113 PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
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      133 CysValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 152
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      153 AlaCysAlaValAlaValIleIleIleIleIleIleIleIleIleIleIleIleIle 172
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      1208 CCACAGACCGTGCAGACCAACACACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1267
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      1268 TCCACAC-----CATGCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1315
      212 ValIleValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 231
      1316 ATCACCACGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1375
      232 AspSerCysLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 251
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      252 ValCysPheLeuProIleIleIleIleIleIleIleIleIleIleIleIleIleIle 270
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      1496 GGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1555
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RESULT 13
US-09-088-337B-43

Sequence 43, Application US/09088337B
Patent No. 6348574

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald

Gray, Patrick W.
Schweikart, Vicki L.

TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
            Borun
            STREET: 6300 Sears Tower, 233 South Wacker Drive
            CITY: Chicago
            STATE: Illinois
            COUNTRY: USA
            ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-088-337B-43
Alignment Scores:
Pred. No.: 8,55e-31 Length: 1901
Score: 394.50 Matches: 91
Percent Similarity: 51.48% Conservative: 66
Best Local Similarity: 29.84% Mismatches: 135
Query Match: 22.28% Indels: 13
Gaps: 6
US-10-023-775b-2 (1-337) x US-09-088-337B-43 (1-1901)
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      860 TGGCTTTTCATC-----CGAGACCAACAGTCCGGGACCCCGGCAACGATGCTCCTG 910
      73 LeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSerLeuProIleIleIleIle 92
      911 ATGCATCTGGCCCTGGCCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 970
      93 TyrAlaSerGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 112
      971 CACTTCTCTGGAGAACCACTGCGCATTTGGGGAATGCAATGCCGCTCACCGGCTTCTC 1030

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 22:13:19 ; Search time 1746 Seconds

(without alignments)
9405.626 Million cell updates/sec

Title: US-10-023-775b-1

Perfect score: 1014
Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estba:*
2: em_esthu:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
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27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	126.6	12.5	623	14	B0038875 pgnlc.pk0
3	115.8	11.4	641	14	B0396255 NISC-ng19
4	114.8	11.3	638	9	AL675845
5	109.4	10.8	877	12	BG402029
6	108.8	10.7	663	13	BM426517 pgf2n.pk0

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	17	95.6	9.4	851	13	B1833118	B1833118 603090834
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	20	94	9.3	884	9	AL525099	AL525099 AL525099
	21	94	9.3	898	13	B1819396	B1819396 603034571
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	23	93.8	9.3	523	14	B0551383	B0551383 H4008H11-
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	37	87.6	8.6	1057	14	BM918711	BM918711 AGENCOURT
	38	87.6	8.6	2146	11	BC027965	BC027965 Homo sapi
	39	87.2	8.6	529	9	AA177828	AA177828 mt07f02.f
	40	87.2	8.6	585	10	BE627479	BE627479 uuz5207.y
	41	86.8	8.6	570	12	BG579061	BG579061 df122e05.y
	42	86.8	8.5	869	14	BQ724793	BQ724793 AGENCOURT
	43	86.6	8.5	516	9	AL698846	AL698846 DKF2P686P
	44	86	8.5	734	13	BG914321	BG914321 602810633
	45	86	8.5	1082	14	BQ710754	BQ710754 AGENCOURT

ALIGNMENTS

RESULT 1
BM723768
LOCUS 744 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-EOI-aiix-g-16-0-UI.r1 UI-E-EOI Homo sapiens cDNA clone
ACCESSION BM723768
VERSION UI-E-EOI-aiix-g-16-0-UI 5', mRNA sequence.
KEYWORDS BM723768.1 GI:19045099
SOURCE EST.
ORGANISM human.

REFERENCE 1 (bases 1 to 744)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996).
MEDLINE 97044477
COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source

1. 744

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-EO1-16-0-UI"

/clone_11d="UI-E-EO1"

/tissue_type="fetal eye"

/dev_stage="fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldi, Lennon and Sears, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t

ORIGIN

Query Match 24.0%; Score 243; DB 14; Length 744;

Best Local Similarity 100.0%; Pred. No. 3.4e-60;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

772 CATATCTGAGGCGATTCGATCGATTCGCTGCTTCATCATGTTGTCATGAG 831
1 CATATCTGAGGCGATTCGATCGATTCGCTGCTTCATCATGTTGTCATGAG 60
832 AATCAGATCCATGAGCTTACATGTTTACAGCATTTAGCTGCTGGAACCTTTGGT 891
61 AATCAGATCCATGAGCTTACATGTTTACAGCATTTAGCTGCTGGAACCTTTGGT 120
892 AACCTGTTACTATATGTTGTTGTCAGGACACTTTCAGGAGCTGCTGCTCAACAGTG 951
121 AACCTGTTACTATATGTTGTTGTCAGGACACTTTCAGGAGCTGCTGCTCAACAGTG 180
952 AGATGCAAAAGTACCGGAGCCTTGAGCAAGCAAAAGTATGTTACTCAAAACCTT 1011
181 AGATGCAAAAGTACCGGAGCCTTGAGCAAGCAAAAGTATGTTACTCAAAACCTT 240
1012 TGA 1014
241 TGA 243

RESULT 2
B0038875
LOCUS
DEFINITION 623 bp. mRNA. linear. EST 01-MAY-2002
B0038875
B0038875.2 GI:20383637

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
B0038875
B0038875.2 GI:20383637
EST.
chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1. (bases 1 to 623)
AUTHORS Morgan, R.W. and Burnside, J.
TITLE Chicken Lymphoid ESTs
JOURNAL Unpublished (2001)
COMMENT On Mar 27, 2002 this sequence version replaced gi:19772415.

CONTACT

Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302 831-3411
Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES

source

1. 623

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="pNICD.113"

/clone_11d="normalized chicken lymphoid cDNA library"

/sex="Male and Female"

/tissue_type="thymus, bursa, spleen, PBL, bone marrow"

/lab_host="E. coli EMD10B"

/note="Vector: PCMVSPORT 6"

BASE COUNT 117 a 199 c 172 g 128 t 7 others

ORIGIN

Query Match 12.5%; Score 126.6; DB 14; Length 623;

Best Local Similarity 53.6%; Pred. No. 5.8e-26;

Matches 258; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

92 TCAGATGACACTTACCTCCCTGTTATATGATATATCTTCCTGCGGATTTCCAGCA 151
124 TCAGATGACACTTACCTCCCTGTTATATGATATATCTTCCTGCGGATTTCCAGCA 183
152 ATGACAGTATGATATATGATATATGATATATGATATATGATATATGATATATGAT 211
184 ACAGCGTGGCATCTGATATGATATGATATGATATGATATGATATGATATGATATGAT 243
212 TTAGCTGAACTGCGCTGCAAGATCTGATATGATATGATATGATATGATATGATATGAT 271
244 ACATGTTCAACCTGCTGCTGCGGACATCTGATATGATATGATATGATATGATATGAT 303
272 ACTATGATGACAGTGGGAAACTGATCTTTGAGATTTCAATGATATGATATGATATGAT 331
304 TCTACTACTTCAACAAACACCTGATGATCTTGGGAGCTGATGATGATGATGATGATGAT 363
332 TCAGCTGATTTCAACCTGATATGATATGATATGATATGATATGATATGATATGATATGAT 391
364 TCAATTTTCCACGTAACCTTACGAGCATCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 423
392 GCTACTGTTGATCATTTACCAATGAGTCTTTTCCATTCACAAATCGATGTCAG 451
424 GTACACGGGCGTGTGTCACACCGCTGTAAGTGTGTTGGGAGCTGTAAGTAAGTAAG 483
452 TTGAGCTGCTGCTGTTGTTGATATGATATGATATGATATGATATGATATGATATGAT 511
484 TGTACGTACCTGCTGCTGTTGTTGATATGATATGATATGATATGATATGATATGATATGAT 543
512 TGATCATCATCAACCAACGAGCAACAGATGATGATGATGATGATGATGATGATGATGAT 571
544 ACTCAGGAGCAGNNNGTAGAGGAGCAAAACCATCAGTGTCTTCTTCTTCTTCTTCTTCTTCT 603
572 A 572
604 A 604

RESULT 3
B0396255
LOCUS
DEFINITION 641 bp. mRNA. linear. EST 22-MAY-2002
B0396255
B0396255.1 GI:21083932
EST.
chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

KEYWORDS	REFERENCE	JOURNAL	COMMENT
EST	NIH-XGC	NIH-XGC	NIH-XGC
western clawed frog.	http://image.llnl.gov/image/html/xenopuslib_info.shtml	http://image.llnl.gov/image/html/xenopuslib_info.shtml	http://image.llnl.gov/image/html/xenopuslib_info.shtml
Silurana tropicalis	Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Silurana.	National Institute of Child Health and Human Development, National Cancer Institute, Xenopus Gene Collection	Unpublished (2002)
1 (bases 1 to 641)			
132 a	184 c	153 g	172 t
BASE COUNT	132 a	184 c	153 g
ORIGIN	132 a	184 c	153 g
Query Match	11.4%;	Score 115.8;	DB 14; Length 641;
Best Local Similarity	51.7%;	Pred. No. 8.9e-23;	
Matches	264;	Conservative	0; Mismatches 247; Indels 0; Gaps 0;
92	TCAAGATGACCTACCTCCCTGTTATTTATGCAATTTCTCCCTGGGATTCACAGCA	151	
125	TCAAGTACGTCCTCTCCCTCCCTGTCGTCAGCGATCATCTGTTCTGGTGGGCTGATTCGTA	184	
152	ATGCAATGATGATATTCACCTACATTTTCAAAATGAGACGCTTGGAAAGACGACACCATCA	211	
185	ACATTTCTGGCCCTGTACATCTTCTCTGTCGGATCAAGCCCTGGAAACGCTTCACACCATC	244	
212	TTATGCTGAACCTGGCGTCACAGATGCTGTATCTGATCTGACAGCCTCCCTTCCTGATTC	271	
245	ACATGTTACACCTGGCCATTTCCGACATGATGATGATGATGATGATGATGATGATGATGATG	304	
272	ACTACTATGACAGTGGCGAAATCTGGATCTTTTGGAGATTTGATGATGATGATGATGATG	331	
305	ATTACTACTCTCGAAGGGGAGCAACATGCGCTTGGCGGCTTGGCGGCTTGGCGGCTTGG	364	
332	TCAGTTCACATTTCAACTGTATATGACAGCATCTTCTTCACACCTGTTTACAGCATCTTC	391	
365	TCCTTTTCTTACACCAACATGTATGATGATGATGATGATGATGATGATGATGATGATGATG	424	
392	GCTACTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	451	
425	GCTTCTCTGGGATCTGCTACCATGATGATGATGATGATGATGATGATGATGATGATGATG	484	
452	TTGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	511	
485	GGATATATTTCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	544	
512	TGATGACATCAACCAACGACCAACAGATGATGATGATGATGATGATGATGATGATGATG	571	
545	TTGTTTACACCAAGTTCCAAATGGGAGGACACACACCTGACATGACATGACATGACATG	604	

Oy	572 AACCTAATACATTAAAGTGGTAGCAACCATAAT	602
Dd	TATTGACAACCTTGTTGGTTACAGCACAGT	635
RESULT 4		
LOCUS	AL675845	638 bp mRNA linear EST 18-MAR-2002
DEFINITION	AL675845 XGC-gastrula Silurana tropicalis cDNA clone Tgas05in19 5'	
ACCESSION	AL675845	
VERSION	AL675845.1	GI:19532219
KEYWORDS	EST.	
SOURCE	western clawed frog.	
ORGANISM	Silurana tropicalis	
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Ambiphila; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;	
	Xenopodinae; Silurana.	
	1 (bases 1 to 638)	
REFERENCE	Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.	
AUTHORS	Sanger Xenopus tropicalis EST project 2002	
TITLE	Unpublished (2001)	
JOURNAL	Contact: Taylor R	
COMMENT	Sanger Centre Hinxton, Cambridgeshire, CB10 1SA, UK Email: tropesanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPOCALIS_SEQUENCE_ID: Tgas05in19.plcsp6 Sequencing primer: PLCSP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. Location/Qualifiers 1..638 /organism="Silurana tropicalis" /db_xref="taxon:8364" /clone="TGas05in19" /clone_lib="XGC-gastrula" /dev_stage="gastrula (stages 10.5-13 mixed)" /lab_host="Escherichia coli XL1-blue" /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI. cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."	
FEATURES		
Source		
BASE COUNT	134 a 180 c 144 g 179 t	1 others
ORIGIN		
Query Match	11.3%; Score 114.8; DB 9; Length 638;	
Best Local Similarity	51.5%; Pred. No. 1.7e-22;	
Matches	263; Conservative 0; Mismatches 248; Indels 0; Gaps 0;	
Oy	92 TCAGATCAGCTACTCCCTCGTTATTATAGCATTAATCTTCCTCGTGGGATTTCCAGCA	151
Dd	121 TCAAGTAGCTCTCCCTCCCCTGCCGTGCTAGGCAATCGTCTTCGCTGGGGCTGAATCCA	180
Oy	152 ATGAGATGTGATATCCACTATACATTTCAAATGAGACTGTGGAAGAGCAGCAACATCA	211
Dd	181 ACATTCTGGCCCTGTACATCTTCCCTGTTCCGGATCAACCCCTGGAAGCCCTCCACACT	240
Oy	212 TTATGCTAGAACCTGGCCGTGACAGATTCGTATATCTGATCTGACAGCCCTCCCTCGATT	271
Dd	241 ACAATGTCACACCTGGCCCAATTCGCGACATGATAGCTGATCCCTCCCGGTGGTGCCT	300
Oy	272 ACTATATGCAAGTGGGCAAAACGTGGATCTTTGGAGATTTATGTATGTTATTCCT	331
Dd	301 ATTACTATCCAGGGGAGCAACATGCGCTTGGGGTGGCTTTGGCAAGATCGCAAGT	360
Oy	332 TCAGCTTCATTTCAACCTGTATAGCAGCAATCTTCCTCAACCTGTTTACAGATCTCC	391
Dd	361 TCCTTTTTACACCAACAATGATAGCTAGCATCTCCTTTTGGTGTGATCAGATCCACAC	420
Oy	392 GCTACTGTGTGATCATTCACCCCAATAGAGCTGCTTTTCATTACAAAACTGATGTGAG	451

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Db      421 GCTTCCTGGGATGCTGTACCCAAATGAAATCAGTGGTGGAGTGGGAATGCTC 480
Qy      452 TTGAGCCTGTGCTGTGATGATCATTCATGATGCTGATTCATTCGATGACCTTCT 511
Db      481 GGAATATTCGCGTGTGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy      512 TGATCATCATACCAACAGACAGACAGATCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 571
Db      541 TTGTTACCAACAGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy      572 AACCATACCTATTAAGTGTACACCTAAT 602
Db      601 TATTGACAACCTGTTGTCTACAGCAAGT 631

RESULT 5
BG402029
LOCUS    877 bp      mRNA      linear      EST 12-MAR-2001
DEFINITION 602466748F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4594810 5',
            mRNA sequence.
ACCESSION BG402029
VERSION   BG402029.1 GI:13295477
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE     NIH-MGC http://mgc.ncl.nih.gov/
COMMENT    National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaaps-remail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            plate: LICM1336 row: p column: 11
            High quality sequence stop: 542.
            Location/Qualifiers
                1..877
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4594810"
                /clone_1lb="NIH_MGC_75"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1:
                SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CACGCGCATATGCGC-3' and 3' adaptor sequence:
                5'-ATTCTAGAGCGCGAGCGCGCGACATG-dT(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.65
                kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH_MGC library."
BASE COUNT 198 a      221 c      199 g      259 t
ORIGIN
Query Match 10.8%; Score 109.4; DB 12; Length 877;
Best Local Similarity 58.5%; Pred. No. 7; 9e-21;
Matches 210; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy      55 GCTGCTTTGGAAATTCAGCTGATGAAAATCCATCCATGAGTGCATCTCCCTGTT 114
Db      125 GCAACTTGCAGAAAACGTGGCGACAGAGCGCTCGCCCTGAAAAGTACTCTTCATTT 184
Qy      115 ATTATGCAATTCCTTCCTCGTGGGATTTCCAGGCAATGCACTAGTATTCACCTTAC 174

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Db      185 TTTATGGGATGATGCTGCTGTGGAGTCCCTGGAAAATACCATTTGTTTACGCTTAC 244
Qy      175 ATTTTCAAAAATGAGACCTTGGAGAGACAGACACATCATTTATGCTGACACTGGCTGCACA 234
Db      245 ATCTTCCTCTGGAAGAACTGGAAACAGAGATATTTATCTCTTTAACCTCTCTGCTCT 304
Qy      235 GATCTGCTGATCTGAGACAGCTCCCTGCTGATTCAGTACATGACCAAGTGGGAAAAC 294
Db      305 GACTTACCTTTCTGTCGACACCTCCCATGCTGATTAAGAGATATGCAAAATG---AAAC 361
Qy      295 TGGATCTTTGAGATTCATGATTAAGTTATCCGCTTACGCTTCATTTCAACCTGTAT 354
Db      362 TGGATATATGAGAGAGAGCTGCTGCATAGACCAATATGCTTCAATGCAACCTGTAT 421
Qy      355 AGCAGATTCCTCTCTACCTGCTTTCAGATCTTCGCTACGTGTGATCATTCACCC 413
Db      422 ACCAGCATTTCTCTTCTTACCTTTATTCAGCATAGATGATATTAAGTATCC 480

RESULT 6
BM426517
LOCUS    663 bp      mRNA      linear      EST 30-JAN-2002
DEFINITION pgf2n.pk002.06 Normalized Chicken Abdominal Fat Library (pgf2n)
            Gallus gallus
ACCESSION BM426517
VERSION   BM426517.1 GI:18430913
KEYWORDS  EST.
SOURCE    chicken.
ORGANISM  Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
TITLE     1 (bases 1 to 663)
COMMENT    Cogburn, L.A., Morgan, R. and Burnside, J.
            ESTs from Normalized Chicken fat cDNA library-USDA/IFARS Animal
            Genome Project
            Unpublished (2002)
            Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburnudel.edu, www.chickest.udel.edu.
            Location/Qualifiers
                1..663
                /organism="Gallus gallus"
                /strain="Commercial broiler, Ottawa Research Centre,
                leghorn"
                /db_xref="taxon:9031"
                /clone="pgf2n.pk002.06"
                /clone_1lb="Normalized Chicken Abdominal Fat Library
                (pgf2n)"
                /sex="Male and Female"
                /tissue_type="Abdominal Fat"
                /dev_stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9
                ,w16,lyr)"
                /lab_host="E. coli EMD10B"
                /note="Vector: pCMVSPORT6; Library made from equivalent
                pools of total RNA isolated from each developmental age
                (across strains); Single pass sequencing from 5'-end"
BASE COUNT 102 a      223 c      210 g      121 t
ORIGIN
Query Match 10.7%; Score 108.8; DB 13; Length 663;
Best Local Similarity 57.5%; Pred. No. 1e-20;
Matches 188; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

Qy      92 TCAAGATGCATACCTCCCTGTTATTTATGCAATTCCTCTGCTGGATTTCCAGGCA 151

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Db 335 TCCAGTTCACACTACGCCACCCTCTACATCCTCTTCATACACCGGGTCTTGAGCA 394

OY 152 ATGACGTAGTATGATACCTTACATTTTCAAAATGAGACTTGAGAGACAGCATCA 211

Db 395 AAGCGTGGCCATCTGATGATGCTTCTTCCACATGCGCGGAGCGGATCTCGGT 454

OY 212 TTATGTCGACCTGGCCCTGACAGATCTCTGTATGACAGCCCTCCCTTCTGATTC 271

Db 455 ACATGTTCAACCTGGCTGGCGGACTCTCTGTATGCTCTCAGCGCCGCCCTCATCT 514

OY 272 ACTACATGCGACGTGGCGAAACGTGATTTTGAGATTTCAATGTGTAAGTTATCCGCT 331

Db 515 TCTACTACTTCAACAAACCGACCTGTGCGGAGCGCATGTGCAAGCTGCAGAGGT 574

OY 332 TCAGCTTCATTTCAACCTGTATGAGAGATCCTCTCTGCAACCTTTTCAGCATTC 391

Db 575 TCAATTTTCAACGTGAACTCTACGCGAGATCTCTNNCTCAGTGCATTAAGCGTNNCA 634

OY 392 GCTACTGTGTGATTCATTCACCCATGA 418

Db 635 GGATATCGGGCGCTCGTNNCCGCTGA 661

RESULT 7

CNS0532S/c 1101 bp DNA linear GSS 26-JUL-2000

LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone 020M21 of library A from Tetradon nigroviridis, genomic survey sequence.

ACCESSION AL318925

VERSION AL318925.1 GI:9551809

KEYWORDS GSS: genome survey sequence.

SOURCE Tetradon nigroviridis.

ORGANISM Tetradon nigroviridis.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradon.

1 (bases 1 to 1101)

Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Winker, P., Brotlier, P., Quetier, F., Saurin, W., and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE 20296633

REFERENCE PUBMED 10835645

REFERENCE AUTORS 2 (bases 1 to 1101)

Crolius, H., Jallion, O., Dasilva, C., Ouzouf-Costaz, C., Fizames, C., Bernot, A., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Fischer, C., and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

MEDLINE 20359837

REFERENCE PUBMED 10899143

REFERENCE AUTORS 3 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (12-APR-2000)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetradon>.

FEATURES

source

1..1101

Location/Qualifiers

/organism="Tetradon nigroviridis"

/db_xref="taxon:99883"

/clone="020M21"

/clone_1lb="A"

/note="Genoscope sequence ID : COAA020AG11C1-end : T7"

BASE COUNT 305 a 216 c 280 g 284 t 16 others

ORIGIN

Query Match 10.6%; Score 107.4; DB 17; Length 1101;

Best Local Similarity 54.0%; Pred. No. 3.4e-20;

Matches 258; Conservative 0; Mismatches 216; Indels 4; Gaps 2;

OY 92 TCAAGATGACACTACCTCCCTGTTATTTATGAGCATATTCCTCTGAGGATTTCCAGGCA 151

Db 507 TCAAAATACATCCCTCCGCGCTGCTCTATGAGCCCTGCTGTCTGCTGCTTATCTCA 448

OY 152 ATGCACTAGTATGATTCACCTTACATTTTCAAAATGAGACCTTGGAGAGAGACCATCA 211

Db 447 ACGCCACAGGCCCTGT---GGCTCTTCTGAGATGCGGCCCTGGAACCCACACACCGCT 391

OY 212 TTATGTCGAAACCGGCGCTGACAGATCTGTGTATGACACACCCCTCCCTTCATTC 271

Db 390 TCTTGTTCACCTCGGCGCTCTCCGACTTCTCTCAATCTGTGCGGTGCCACCTCATCT 331

OY 272 ACTACTATGCGACGTGGCGAAACGTGATCTTTGAGATTTCAATGTATGATTTATCCGT 331

Db 330 ACTATTACGCCAACACAGGCGCACTGG-CCTTGGCGTGGGAGCGCTGCAAAATGTGGCT 272

OY 332 TCAGCTTCATTTCAACCTGTATGAGAGATCCTCTTCTGACCTGTTTCAGCATCTTC 391

Db 271 TCCCTTCTTACGTCACACTCTACTGCGAGATCTCTTCTTCCATCCTCATCAGCGGTAC 212

OY 392 GCTACGTGTGATTCATTCACCCATGAGAGTCTTTCATTCACAAACCGATGCGAG 451

Db 211 GTTACGTGGCATCTCCACCCGATTAAGCGCTGATCTGTGAANCCCGANATTCCT 152

OY 452 TTGTACCTGTGCTGTGTGTGATTCATTTCACTGTAGCTGATTCGATTCGATACCTCT 511

Db 151 ACCTGGTGTGGCGCTGCGTGTGGTGTGTGTATATGTGTGTGTGTGTGTGTGTGTGT 92

OY 512 TGTATCATTCACCAACAGAGACACAGATACAGCTGTCTGCACTTCCAGCATTCGGA 569

Db 91 TTGTACCACTTCCAGCGGAGCAATATCCCTGTGCATGATTAACACANNGCCGGA 34

RESULT 8

LOCUS BG712193

DEFINITION pglin.p011.f3 Normalized Liver Library Gallus gallus cDNA clone p011.p011.f3 5' similar to g011AC60339.1 (AF031897) 6 protein coupled p2x nucleotide receptor [Meleagris gallopavo]g, mRNA sequence.

ACCESSION BG712193

VERSION BG712193.1 GI:14006135

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 491)

Burnside, J., Morgan, R.W., and Cogburn, L.A.

Chicken ESTs from a normalized liver library

Unpublished (2001)

Contact: Joan Burnside

Molecular Endocrinology

University of Delaware

40 Townsend Hall, Newark, DE 19717, USA

Tel: 302 831-1345

Fax: 302 831-3411

Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES

source

1..491

Location/Qualifiers

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="pglin.p011.f3"

/clone_1lb="Normalized Liver Library"

/sex="Male and Female"

/tissue_type="liver"

/lab_host="E.coli EMDH10B"

ORIGIN

[ANGTGGCCCTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCCTACTG], digested

676 t

ome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
Wagk, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedic: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES

source

1. 422
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="F530201P11"
/clone_lib="RIKEN full-length enriched, adult male kidney"
/sex="male"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="SOLR"
/note="Site_1: XhoI; Site_2: SstI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGCGCCGCACTGAGATTGTTTATTTTATTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGAGATGACGAGCTGATTAATTAATAAACCCCCCC 3'].
cDNA was cleaved with XhoI and SstI."

BASE COUNT

104 a 100 c 88 g 130 t

ORIGIN

Query Match 9.9%; Score 100; DB 10; Length 422;

Best Local Similarity 57.5%; Mismatches 145; Indels 3; Gaps 1;

Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

59 CTTTGGAAATTCAGTGAAGAAACATCCACTCAAGATGACATCCCTGTTATTT 118
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
75 CTGTGAGAAATGTTGGCAACAGAGGCTATCTGATATAGTACTCTCGCATTTT 134
111 111 111 111 111 111 111 111 111 111 111 111 111 111
119 ATGGCATATATCTCCGTCGGGATTTCCAGGCAATGAGATGATATCCACTTATTT 178
111 111 111 111 111 111 111 111 111 111 111 111 111 111
135 ATGCATCGAGCTTATTTTGGACTGCTGGGATGCTACTGTGGTGGTGGTACTCTT 194
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179 TCAGAAATGAGACTTGGAGAGAGCAACATCATTTATGCAAGCTGGCTGACAGATC 238
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195 TCGCATGAGAAAGTGAAGAGCAAGATGCTATCTTTTAACCTTTTCATCTGACT 254
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239 TCGTATATGACACAGCTCCCTCTGATGCTACTATGACAGAGGAGAAACGGA 298
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255 TTGCTTCTGTCGACCTTCCTCATGATTAAGATTAATGCAAT--GATTAAGGGA 311
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312 CCATGAGATGTTCTGTATTAAGCAACGATATGCTTCAACACCACTCTTAACCA 371
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359 GATCTCTCTCTCAGCTGTTGAGCATCTTCGCTACTGTGATCA 406
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372 GATCTCTCTCTCAGCTTCAATGATGAGCCGATATGCTATGCA 419
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RESULT 14
BG924078
LOCUS
DEFINITION
BG924078 801 bp mRNA linear EST 05-JUN-2001
602823635F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4952433 5',
mRNA sequence.

ACCESSION
BG924078
VERSION
KEYWORDS
SOURCE
house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 801)
NIR-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: LRAM10910 row: e column: 10
High quality sequence start: 25
High quality sequence stop: 799.

FEATURES

source

1. 801
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4952433"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT

166 a 228 c 193 g 213 t

ORIGIN

Query Match 9.8%; Score 99.6; DB 13; Length 801;

Best Local Similarity 53.3%; Pred. No. 5.8e-18;

Matches 210; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

102 CTACCTCCGTTATTTATGCAATTCCTCCGCGGAGTTCCAGGCAATGAGT 161
111 111 111 111 111 111 111 111 111 111 111 111 111 111
188 CTTTCTCCGCTGCTCAATTAATGTTGTTGATGTTGGCCAGTATGGATGGC 247
111 111 111 111 111 111 111 111 111 111 111 111 111 111
162 GATATCACTTACATTTTCAAAATGAGACCTTGAAGAGAGCAACATTTATGCTGA 221
111 111 111 111 111 111 111 111 111 111 111 111 111 111
248 CCTCTGATTTCTTTTCGGAAGAGAAAGAAACCCGCGTATTTACATGGCA 307
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308 CCGTGGCTTGGCTGACCTCTCTGTCATCTGTTCCCTGCGCATGCTTACACCG 367
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282 CAGTGGCAAAATGATCTTTGGAATTTCAATGTTAATTCGCTTCAAGCTTCCA 341
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368 ACATGGCAACACTGGCTATGAGGAGGCGCCGCAAGTCTATGGCTTTTCA 427
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342 TTTCACCTGATATGAGAGATCTCTCCGACCTGTTGAGATGCTCCGATGATG 401
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428 TGCAACATGATTTGCTCAATCTCTTTCATGACCTGCTCAGGCTCAGAGATGAG 487
111 111 111 111 111 111 111 111 111 111 111 111 111 111
402 GATCATTCACCAATGAGCTTCTTTCATTCACAAACCTGATGATGATGATGAG 461
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Db 488 GATCGTGAACCCCATGGGACACCCAGAGAACCAATCCGCTGGCTCTCCT 547
462 TCGTGTGTGTGATCATTTACCTGTAGCTGTC 495
Db 548 GGCAATCTGGCTCTCATTTTCTGTGTCACATC 581

RESULT 15

A2953874

LOCUS A2953874 606 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0219L17F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION A2953874

VERSION A2953874.1 GI:13825101

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
'M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0219 row: L column: 17

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 606.

Location/Qualifiers

1. 606

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0219L17"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g114732114[gb]AF129072.1), a copy number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT

ORIGIN

100 a 203 c 145 g 158 t

Query Match

9.7%; Score 98.4; DB 17; Length 606;

Best Local Similarity 57.2%; Pred. No. 1.1e-17;
Matches 199; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

QY 217 CTGAACCTGGGCTGCACAGATGCTGTATGTGACACGCTCCCTCTGTACTATC 276
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Db 220 TATGCGAGTGGGAAACCTGATCTTTGAGATTCATGTGATTTATGCGCTTCAC 279
QY 337 TTCCATTTCAACCTGTATAGACAGATCTCTTCACACCTGTTTCAGCATTTCCGCTAC 396
Db 280 TTCTATGCAATCTATCATGTGACAGCATCTCTTCACACCTGTTTCAGCATTTCCGCTAC 339
QY 397 TGTGTGATCATTCACCAATGAGCTGCTTTTCATTCACAAATCGATGTGCAATTT 453
Db 340 CTGGGCAATCTGCCACCCCTGCTTCCTGGCACAAGCGTGAAGTGGCGCTGCTTGG 399
QY 454 GTAGGCTGTGCTGTGTGTGATCATTTTCACCTGTAGCTGTGATTCGATTCGATTCG 513
Db 400 GTAGTGTGTGAGTATGT 459
QY 514 ATCATATCAACCAACGACGACACAGATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 561
Db 460 GGTGCACATGATCATTCATCGCAACGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 507

Search completed: May 29, 2003, 23:40:16
Job time : 1751 secs

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QY	115	ATTATAGGCAAT	ATCTTCTCTGCTGGGATTTCCAGCAATGCAGTAGATATTCACCTTAC	174
Db	709	TTTTATGGGAT	TGGATCGTTGTGGGATCCCTGGAAATACCAATGTGTGTACGGGCTAC	768
QY	175	ATTTTCAAAAT	TGGACCTTGGAAAGGACGACCAATCATATGATGTAACCTGGCTGCACA	234
Db	769	ATCTTCTCTCTG	AAAGAACTGGAAACGACAGCATATATTTATCTTTAACTCTCTGTCTCT	828
QY	235	GATCTGCTGTAT	TCTGACACAGCCTCCCTCCCTGATCTACTATATGACAGTGGGCAAAAC	294
Db	829	GACTTAAGCTT	TCTGTGTGACACCTCCCACTGTGATTAAGGATTAATGCCAAATGG---	AAAC 885
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Db	886	TGGATATATGAG	ACGTGCTGTGATTAAGCAACGATATGTGCTTATGACCAACTCTAT	945
QY	355	AGCAGATCCCT	CTCCACCTGTTTGAAGATCTTCGCTACTGTGTGATCATTTACCCA	414
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Db	1066	GTTTTATTAAC	CTTAGAGTTACTACCATACTCTCCCTTAATAATCCGTATTAATGAC	1125
QY	535	AACGATCAGC	CTGTCTCGACCTCACCAAGTTCCGATGAACCAATACTATTAAGTGTAC	594
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QY	115	ATTATATGCGATTAT	CTCTCTGTTGGGATTTCCAGGCAATGCAGTGTATATCCACTTAC	174		
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QY	175	ATTTTCAAAATAGAC	CTTGGAAAGCAGCAACCATTTATGCTGAACCTGACCTGCACAA	234		
Db	769	ATCTTCTCTCTGA	AGAACTGGAACAGCAGTATATTTATCTTTAACTCTCTGCTCT	828		
QY	235	GATCTGCTGTATCT	GCAGCAGCCCTCCCTCTCTGATTCATCTATGCGAGTGGCGAAAC	294		
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QY	295	TGATCTTTGGAGAT	TTTCATCTGTATATCCGCTTCAAGCTTCCATTTAACCTGTAT	354		
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QY	355	AGCAGCAGCCCT	CTCCCTCACTGTTTGCATCTTCGCTCTGCTGAGATCATTCACCA	414		
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QY	535	AACGATACAGCT	CTCTGACACTCACCAGTTCGGATGAACATCATATTAATAGTATG	594		
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QY	595	AACCTAATTTT	TGATGCAATCTTTCGCTCCCTTGGATAGTATGATGACACTTTGCTAT	654		
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Db	1246	TACAAAGTTT	GGTCTCTTCTTAACCAAGCAGAGAAATGGAAGTTGCTACTGCTCTGCCCTT	1305		
QY	709	CAGAAAGCAGAG	GGCTATACCATTTCTGCTACTCTTGTGATTTTACGATGTTTTTTTACCC	768		
Db	1306	GAAAGGCTCTCA	CTGATCTGATCATGAGAGTGGATGCTATCTCTCTGCTTTTATACACC	1365		

Matches 222; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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QY 106 CTCCTGTTATTTATGACATATCTCTGCTGGATTTCAGCAATGACATGATGATA 165
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QY 346 AACCTGTATAGACACATCTCTTCTCCTACCTGTTTCAGACATCTTCCGCTACTGTGTATC 405
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b 462 TTACGACCTCTGCGCTCCCTGCGCTGGGCGCGGCTAGCGCTGCGCGGCTGCGCGG 521
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```

RESULT 5

US-08-446-088A-1

Sequence 1, Application US/08446088A

Patent No. 5691156

GENERAL INFORMATION:

APPLICANT: Boucher, Richard C.

APPLICANT: Weisman, Gary A.

APPLICANT: Turner, John T.

APPLICANT: Harden, Thomas K.

APPLICANT: Parr, Claude E.

APPLICANT: Sullivan, Daniel M.

APPLICANT: Erb, Laura

APPLICANT: Lustig, Kevin D.

TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and

TITLE OF INVENTION: Null Cells Expressing P2U Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bell, Seltzer, Park & Gibson

STREET: Post Office Drawer 34009

CITY: Charlotte

STATE: No. 5691156th Carolina

COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,088A

FILING DATE: 19-May-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kenneth D. Sibley

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5470-71C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1842 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 57..1181

US-08-446-088A-1

Query Match 10.2%; Score 103.2; DB 1; Length 1842;

Best Local Similarity 52.9%; Pred. No. 9e-22;

Matches 222; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Db 522 GCGGTGGGTTGTGGTGTGCGCTGCGACAGGCCCGCTGCTGTACTTGTACACACAGC 581
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

```

RESULT 6

US-08-513-974B-41

Sequence 41, Application US/08513974B

Patent No. 6114139

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Hosoya, Masaki

APPLICANT: Fujii, Ryo

APPLICANT: Ohtaki, Tetsuya

APPLICANT: Fukusumi, Shoji

APPLICANT: Ohji, Kazuhito

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

NUMBER OF SEQUENCES: 380

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/513,974B

FILING DATE: 14-SEP-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 370:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1020 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 28..1011
 US-08-513-974B-370

Query Match 9.9%; Score 100; DB 3; Length 1020;
 Best Local Similarity 57.5%; Pred. No. 6.2e-21;
 Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

QY 217 CTGAACCTGGGCTGCACAGATCTGCTATCTGACAGAGCCCTCCCTGATTCACATAC 276
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 Db 223 CTGAACCTGGGCTGCACAGATCTGCTATCTGACAGAGCCCTCCCTGATTCATAC 282
 QY 277 TATGCCAGTGGCGAAATGATCTTGGAGATTTCATGTAGTTATCCGCTGAGC 336
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 Db 283 TAGCCAGAGGGAGACACTGCGCTTGGAGACCTCGCGCTTGTACGCTTCTC 342
 QY 337 TTCCATTGCAACCTGTTAGCAGATCTCTCTCTACCTGTTTACAGCATCTTCCGCTAC 396
 |||||
 Db 343 TTCTATGCCAATCTACATGCGAGCATCTCTCTCTACCTGATAGCTTCCAGCGCTAC 402
 QY 397 TGTGTGATCATTCACCCATGAGCTGTTTCTTCAATCAAAATCGATGCGAGT--- 453
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 Db 403 CTGGGCAATCTGCCACCCCTGGCTCTCTGCGACAGAGGTGGAGGTGCGGCTGTGG 462
 QY 454 GTAGCCTGTGCTGTGTGTGATCATTTCACTGTAGCTGTTCATTCGATGACCTCTTG 513
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 Db 463 GTAGTGTGAGATGCTGTGCTGTGTGACAGCCAGTGCCTGCCAAGGCGAGCTCTT 522
 QY 514 ATCATCAACCAACAGACAGACAGATGACCTCTCTGACCTCACC 561
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 Db 523 GCTGCCACAGGACATCCAGCCACCGCATCTGTGTACGACCTGAGC 570

RESULT 8
 US-08-097-938-1
 Sequence 1, Application US/08097938
 Patent No. 5629174

GENERAL INFORMATION:
 APPLICANT: SUNDELIN, JOHAN
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS
 TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/097,938
 FILING DATE: 26-JUL-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22803-20006.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763
 TELE: 90-4030
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1475 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 232..1416
 NAME/KEY: mat.peptide
 LOCATION: 232
 US-08-097-938-1

Query Match 9.6%; Score 97.8; DB 1; Length 1475;
 Best Local Similarity 52.6%; Pred. No. 3.6e-20;
 Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 91 CTCAAGATGCACTACCTCCCTGTTATTTATGGCATATCTCTCGTGGGATTTCCAGGC 150
 |||||
 Db 442 CTGACCAAGGCTTTCTCCGCTGCTACATTTATGTTGATTTGTTGCCAGT 501
 QY 151 AATGCAATGATGATATTCACCTTACATTTTCAAAATGAGACCTTGAAGAGCAGCAGC 210
 |||||
 Db 502 AATGCAATGAGGCTCTGATCTCTCTTTCGGAAGGAAGAAACACCCGCGTAT 561
 QY 211 ATATATGATGAACTGGGCTGACAGATCTGATCTGATCGACACCTCCCTCTGAT 270
 |||||
 Db 562 TACATGGCAACCTTGCTTGGCTGCTGCTACATTTATGTTGATTTGTTGCCAGT 621
 QY 271 CACTACTATGCACTGCGGAAACTGGATCTTTGAGATTTGATGATTTATTCGCG 330
 |||||
 Db 622 TCTACACACCTACATGCAACACTGATGATGATGATGATGATGATGATGATGAT 681
 QY 331 TTGAGCTTCAATTTCAACCTGATATGAGAGATCTCTCTCTACCTGTTTACATCTTC 390
 |||||
 Db 682 GCGCTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741
 QY 391 CGCTACTGTGATCATTCACACCAATGAGCTTTTCCATTCACAAACTCGATGCA 450
 |||||
 Db 742 AGTACTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 801
 QY 451 GTTGATGCTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 495
 |||||
 Db 802 GCGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846

RESULT 9
 US-08-476-000-1
 Sequence 1, Application US/08476000
 Patent No. 5716789

GENERAL INFORMATION:
 APPLICANT: SUNDELIN, JOHAN
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
 TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476,000

FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/390,301
 FILING DATE: 25-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: ADLER, REID G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 2803-0006.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELETYPE: 90-4030
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1475 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 232..1416
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 232
 US-08-476-000-1

Query Match 9.6%; Score 97.8; DB 1; Length 1475;
 Best Local Similarity 52.6%; Pred. No. 3.6e-20;
 Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

91 CTCAGATGACATCCCTCCCTGTTATTTATGAGATATCTTCCGCGGATTTCCAGGC 150
 442 CTGACACAGGCTCTTTCTCCGGTCGTCACATATATGTGTTGATGGTTGGCCAGT 501
 151 AATGACAGTATGATATCCACTTACATTTTCAAAATGAGACCTTGAAGACAGCACCATC 210
 502 AATGACATGGCCCTCGAGATCTTCCTTTCCGAAGAAAGAAACACCCCGCGATGAT 561
 211 ATTATGCTGAACCTGGCCCTGACAGATCTGCTATCTGACAGCCCTCCCTTCGATG 270
 562 TACATGGCCAACTGGCGCTGGCCGACCTCTCTCTGTCATCTGCTGTTCCCTGAGATC 621
 271 CACTACTATGACAGTGGCGAAACTGGATCTTTGGAGATTTCATGTAAGTTATTCGCC 330
 622 TCCTACCACTAATATGCAAACTGGGTCTAGGGGAGGCCCTGTGCAAGGTGCTATT 681
 331 TTCAGCTTCATTTCAACCTGTATAGAGAGATCCTCTTCTCACTGTTTTCAGACTTC 390
 682 GGCCTTTTCTATGTAATGATGATGCTCATCTCTTCAATGACCTGCTCAGGTCAG 741
 391 CGCTACTGTGTATCATTCACCCCAATGAGCTGCTTTTCCATTACAAAATCGATGCA 450
 742 AGGTACTGGGTGATCGGAACCCCATGGGACCCCAAGGAAGCAATCGCGTT 801
 451 GTTGTAGCCCTGCTGTGCTGATCATTTCACTGCTGATCTGTC 495
 802 GCGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTCACATC 846

RESULT 10
 US-08-472-840-1
 Sequence 1, Application US/08472840
 Patent No. 5763575
 GENERAL INFORMATION:
 APPLICANT: SUNDELIN, JOHAN
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
 TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,840
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,301
 FILING DATE: 25-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: ADLER, REID G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 2803-0006.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELETYPE: 90-4030
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1475 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 232..1416
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 232
 US-08-472-840-1

Query Match 9.6%; Score 97.8; DB 1; Length 1475;
 Best Local Similarity 52.6%; Pred. No. 3.6e-20;
 Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

91 CTCAGATGACATCCCTCCCTGTTATTTATGAGATATCTTCCGCGGATTTCCAGGC 150
 442 CTGACACAGGCTCTTTCTCCGGTCGTCACATATATGTGTTGATGGTTGGCCAGT 501
 151 AATGACAGTATGATATCCACTTACATTTTCAAAATGAGACCTTGAAGACAGCACCATC 210
 502 AATGACATGGCCCTCGAGATCTTCCTTTCCGAAGAAAGAAACACCCCGCGATGAT 561
 211 ATTATGCTGAACCTGGCCCTGACAGATCTGCTATCTGACAGCCCTCCCTTCGATG 270
 562 TACATGGCCAACTGGCGCTGGCCGACCTCTCTCTGTCATCTGCTGTTCCCTGAGATC 621
 271 CACTACTATGACAGTGGCGAAACTGGATCTTTGGAGATTTCATGTAAGTTATTCGCC 330
 622 TCCTACCACTAATATGCAAACTGGGTCTAGGGGAGGCCCTGTGCAAGGTGCTATT 681
 331 TTCAGCTTCATTTCAACCTGTATAGAGAGATCCTCTTCTCACTGTTTTCAGACTTC 390
 682 GGCCTTTTCTATGTAATGATGATGCTCATCTCTTCAATGACCTGCTCAGGTCAG 741
 391 CGCTACTGTGTATCATTCACCCCAATGAGCTGCTTTTCCATTACAAAATCGATGCA 450
 742 AGGTACTGGGTGATCGGAACCCCATGGGACCCCAAGGAAGCAATCGCGTT 801
 451 GTTGTAGCCCTGCTGTGCTGATCATTTCACTGCTGATCTGTC 495
 802 GCGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTCACATC 846

RESULT 11
 US-08-476-976-1

```

: Sequence 1, Application US/08476976
: Patent No. 5874400
: GENERAL INFORMATION:
: APPLICANT: SUNDELIN, JOHAN
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
: TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/476,976
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/390,301
: FILING DATE: 25-JAN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: ADLER, REID G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 2803-0006.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1475 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 232..1416
: NAME/KEY: mat-peptide
: LOCATION: 232
: US-08-476-976-1

```

Query Match 9.6%; Score 97.8; DB 2; Length 1475;
 Best Local Similarity 52.6%; Pred. No. 3.6e-20;
 Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

```

Y 91 CTGAGATGCACTACCTCCCTGTTATTTAGGCAATTCCTCCGCGGGATTTCCAGGC 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 CTGACCCAGGCTCTTTCGCGTCTACATTAATGTTGGATTGGTTGCCAGT 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 AATGCACTAGTATGATTCACCTTACATTTTCAAAATGAGACCTTGAGAGAGCAGCATC 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 502 AATGCAATGGCCCTCTGATCTCTTTTCGAAAGAGAAAGAAACACCCGCCGTCATT 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 AATATGCTGAACCTGGCTGCGACAGATCTGCTGATCTGACCACTCCCTTCGATT 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 562 TACATGCGCAACGCTGGCTGGCGACCTCCTCTGTCATCTGTTCCCTCGAAGATC 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 CACTACTATGCGCACTGGCGAAACTGATCTTTGGAATTTCAATGTAAGTTATCCGC 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 TCTACACCTTACATGGAACCAACTGGCTTACGAGGAGGCCCTGCCAAGTGCCTATT 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 TTGAGCTTCATTTACACCTGATATAGAGAGATCCTCTCCCACTTTTCAGCATCTTC 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 682 GGCCTTTTCTATGTAACATGATTTGCTCCATCTCTTCATGACGCTCCAGGCTCAG 741
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 391 CGTACTGTGATCATTCACCCAAATGAGCTGCTTTTCATTCACAAAATCTGATGCA 450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 742 AGTACTGGTGATCGTGAACCCCATGAGACACCCAGAGAAAGGCAACATGCGCGTT 801
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 GTTGAGCGCTGCTGCTGATGATCATTTTCACCTGAGAGTGC 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 802 GCGCTCTCTTGCAATCTGCTCTCTGATTTTCTGGTACCATC 846
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 12
 US-08-474-410-1
 : Sequence 1, Application US/08474410
 : Patent No. 6043212
 : GENERAL INFORMATION:
 : APPLICANT: SUNDELIN, JOHAN
 : APPLICANT: SCARBOROUGH, ROBERT M.
 : TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
 : TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MORRISON & FOERSTER
 : STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20006-1812
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/474,410
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/390,301
 : FILING DATE: 25-JAN-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: ADLER, REID G.
 : REGISTRATION NUMBER: 30,988
 : REFERENCE/DOCKET NUMBER: 2803-0006.20
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 887-1500
 : TELEFAX: (202) 887-0763
 : TELEX: 90-4030
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1475 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 232..1416
 : NAME/KEY: mat-peptide
 : LOCATION: 232
 : US-08-474-410-1

Query Match 9.6%; Score 97.8; DB 3; Length 1475;
 Best Local Similarity 52.6%; Pred. No. 3.6e-20;
 Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

```

QY 91 CTGAGATGCACTACCTCCCTGTTATTTAGGCAATTCCTCCGCGGGATTTCCAGGC 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 CTGACCCAGGCTCTTTCGCGTCTACATTAATGTTGGATTGGTTGCCAGT 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 AATGCACTAGTATGATTCACCTTACATTTTCAAAATGAGACCTTGAGAGAGCAGCATC 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 502 AATGCAATGGCCCTCTGATCTCTTTTCGAAAGAGAAAGAAACACCCGCCGTCATT 561
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 AATATGCTGAACCTGGCTGCGACAGATCTGCTGATCTGACCACTCCCTTCGATT 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 562 TACATGGCAACCTGGCCCTTGGCCGACCTCTCTGTATCTGTGTTCCCGCCGAGATC 621
QY 271 CACTACTATGCCAGTGGCCGCAAACTGGATCTTGGAGATTTCATGTGTAAGTTATCCG 330
Db 622 TCCCTACACCTACATGCAACCACTGGGCTTACGGGAGGCCCTGTGCAAGGTGCATT 681
QY 331 TTCAGTTCATTTCAACCTGATATAGACATCTCTCTCCACCTGTTTACAGATCTTC 390
Db 682 GGCCTTTTCTATGTATACATGTATTTGCTCCATCTCTTTCATGACCTGCTGACG 741
QY 391 CGCTACTGTGTATCATTCATCCCAATGAGCTGCTTTTCATTCACAAACTGCATGCA 450
Db 742 AGGTACTGGGTGATCGTGAACCCCATGGGACACCCAGGAAGAAGCAATCGCGCT 801
QY 451 GTTGAGCTGTCTGTGTGTGTGATCATTTCTACCTGGTACCTGTC 495
Db 802 GGGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTCACATC 846

RESULT 13

US-08-486-673B-1
; Sequence 1, Application US/08486673B
; Patent No. 6297026
; GENERAL INFORMATION:
; APPLICANT: Sundell, Johan
; TITLE OF INVENTION: Nucleic Acids Encoding the C140 Receptor
; FILE REFERENCE: 44481-5006-08-05
; CURRENT APPLICATION NUMBER: US/08/486,673B
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/097,938
; PRIOR FILING DATE: 1993-07-26
; PRIOR APPLICATION NUMBER: PCT/US94/08536
; PRIOR FILING DATE: 1994-07-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1416)
; OTHER INFORMATION: C140 receptor, genomic DNA and deduced protein
US-08-486-673B-1

Query Match 9.6%; Score 97.8; DB 4; Length 1475;

Best Local Similarity 52.6%; Pred. No. 3.6e-20;

Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 91 CTCAGATGACACTCTCTCTGTTATTTATGCAATATCTCTCTGCGATTTCCAGGC 150
Db 442 CTGACCACTGCT 501
QY 151 AATGAGTATGATATTCATTTCAAAATGAGACTTGGAGAGACAGACATC 210
Db 502 AATGAGTATGATATTCATTTCAAAATGAGACTTGGAGAGACAGACATC 561
QY 211 AATGAGTATGATATTCATTTCAAAATGAGACTTGGAGAGACAGACATC 270
Db 562 TACATGGCAACCTGGCCCTTGGCCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 621
QY 271 CACTACTATGCCAGTGGCCGCAAACTGGATCTTGGAGATTTCATGTGTAAGTTATCCG 330
Db 622 TCCCTACACCTACATGCAACCACTGGGCTTACGGGAGGCCCTGTGCAAGGTGCATT 681
QY 331 TTCAGTTCATTTCAACCTGATATAGACATCTCTCTCCACCTGTTTACAGATCTTC 390
Db 682 GGCCTTTTCTATGTATACATGTATTTGCTCCATCTCTTTCATGACCTGCTGACG 741
QY 391 CGCTACTGTGTATCATTCATCCCAATGAGCTGCTTTTCATTCACAAACTGCATGCA 450

Db 742 AGGTACTGGGTGATCGTGAACCCCATGGGACACCCAGGAAGAAGCAATCGCGCT 801
QY 451 GTTGAGCTGTCTGTGTGTGTGATCATTTCTACCTGGTACCTGTC 495
Db 802 GGGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTCACATC 846

RESULT 14

US-08-476-000-60
; Sequence 60, Application US/08476000
; Patent No. 5716789
; GENERAL INFORMATION:
; APPLICANT: SUNDELL, JOHAN
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390,301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2732 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1269
US-08-476-000-60

Query Match 9.6%; Score 97.8; DB 1; Length 2732;

Best Local Similarity 52.6%; Pred. No. 5.1e-20;

Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 91 CTCAGATGACACTCTCTCTGTTATTTATGCAATATCTCTCTGCGATTTCCAGGC 150
Db 295 CTGACCACTGCT 354
QY 151 AATGAGTATGATATTCATTTCAAAATGAGACTTGGAGAGACAGACATC 210
Db 355 AATGAGTATGATATTCATTTCAAAATGAGACTTGGAGAGACAGACATC 414
QY 211 AATGAGTATGATATTCATTTCAAAATGAGACTTGGAGAGACAGACATC 270
Db 415 TACATGGCAACCTGGCCCTTGGCCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 474
QY 271 CACTACTATGCCAGTGGCCGCAAACTGGATCTTGGAGATTTCATGTGTAAGTTATCCG 330

Db 475 TCCTACCACTACATGGCAACACTGGGTCTACGGGGGAGGCCCTGTGCAAGGTGCTCATTT 534
| | | | |
Qy 331 TTCAGCTTCATTTCAACCTGTATAGCAGCATCCCTCCACCTGTTTACAGATCTTC 390
| | | | |
Db 535 GGCCTTTTCTATGGTACATATATGCTCCATCTCTTCATGACCTGCTTAGCGTGAG 594
| | | | |
Qy 391 CGCTACTGTGTGATCATTACCCCAATGAGCTGTTTCCATTCACAAAACCTGATGTGCA 450
| | | | |
Db 595 AGGTACTGGGTGATCGTAACCCCATGGGACACCCAGGAAGAGCAACATGCGCGTT 654
| | | | |
Qy 451 GTTGTAGCCTGTGCTGTGTGTGTGATCATTTTCACTGGTAGCTGTC 495
| | | | |
Db 655 GCGCTCTCTTGCAATCTGGCTCTGATTTTCTGGTACACATC 699
| | | | |
RESULT 15
US-08-472-840-60
Sequence 60, Application US/08472840
Patent No. 5763575
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,840
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 2732 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1269
US-08-472-840-60
Query Match 9.6%; Score 97.8; DB 1; Length 2732;
Best Local Similarity 52.6%; Pred. No. 5.1e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
Qy 91 CTCAGATGCACTACCTCCCTGTTATTATGACATTAATCTCTCGTGGGATTTCAGGC 150
| | | | |
Db 295 CTGACACAGGCTCTTCTCCGCTGCTACATTTATGTGTGTGTGATGTTGCCAGT 354
| | | | |
Qy 151 AATGCAATGATATACACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATC 210
| | | | |

Db 355 AATGGCATGGCCCTCTGATCTCTTTTCGAAACGAAAGAAACACCCCGCGTGATT 414
| | | | |
Qy 211 AATAGCTGAACCTGGCCCTGCAGCAATCTGATATGACACAGCTCCCTTCCTGATT 270
| | | | |
Db 415 TACATGGCAACCTGGCCCTTGCCGACCTCTCTCTGATCTGTTCCCTCAAGATC 474
| | | | |
Qy 271 CACTACTATGCACTGGGGAACCTGATCTTTGGAGATTTTCATGTGTAACTTATCGC 330
| | | | |
Db 475 TCCTACCACTACATGGCAACACTGGGTCTACGGGGGAGGCCCTGTGCAAGGTGCTCATTT 534
| | | | |
Qy 331 TTCAGCTTCATTTCAACCTGTATAGCAGCATCCCTCCACCTGTTTACAGATCTTC 390
| | | | |
Db 535 GGCCTTTTCTATGGTACATATATGCTCCATCTCTTCATGACCTGCTTAGCGTGAG 594
| | | | |
Qy 391 CGCTACTGTGTGATCATTACCCCAATGAGCTGTTTCCATTCACAAAACCTGATGTGCA 450
| | | | |
Db 595 AGGTACTGGGTGATCGTAACCCCATGGGACACCCAGGAAGAGCAACATGCGCGTT 654
| | | | |
Qy 451 GTTGTAGCCTGTGCTGTGTGTGTGATCATTTTCACTGGTAGCTGTC 495
| | | | |
Db 655 GCGCTCTCTTGCAATCTGGCTCTGATTTTCTGGTACACATC 699
| | | | |

Search completed: May 29, 2003, 23:41:32
Job time : 66 secs

Alignment Scores:

Refd. No.: 1.5e-158 Length: 1014
 Seqre: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775B-2 (1-337) x US-10-023-775B-1 (1-1014)

QY 1 MetLsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 1 ATGATAGGCGACCTAGCATTTATAGCAATGCTTCTGATTTCCCGATATAGCATGCT 60
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTTCGAATTCGACGTGAGAAACATCCACTCAAGATGCACTGCTCCGTATATTTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTTACTCTCCGCGGGATTTCCAGGCAATGCAATGATATCCACTTATTTTC 180
 QY 61 LysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGAGAGACGACACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyAsnTrrPle 100
 DB 241 CTGATCTGACGACCTTCCTCTCGATTCATCTACTATGCGAAGGGGAAACCTGGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTTCGAGATTCAGTGTGATGATATGCGCTTACGCTTCATTCACCTGATATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
 DB 361 ATTCCTCTCTCCACTGTTTCAGCATTTTCCTGCTACTGTCATTCACCATGAGC 420
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaCysAlaValIleTrrPleIle 160
 DB 421 TGCCTTTCATTCACAAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 161 SerLeuValAlaValIleProMetThrPheIleIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCATGTCGATGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrrPyrAsnLeu 200
 DB 541 TCAGCTGCTGTCGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTGACTGCACTACTTCTGCTCTCCCTGGATGATGATGATGATGATGATGATGATG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlyAlaArg 240
 DB 661 ATTTATCCACTGTCGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTAACCATTCGCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnIle 280
 DB 781 AGGCTCATTCGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleLeuAsnThrPheGlyAsnLeu 300
 DB 841 CATGAGCTTACATGCTTCTGACCATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 301 LeuTyrValValIleSerAspAsnPheGlnIleAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGT 960

QY 321 ValSerGlyAsnLeuGlnAlaIleAlaLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAAAGCGGAACTTGTGAGCAAGCAAGCAAAATTAATGTTACTTCAACCAACCT 1011

RESULT 2
 US-10-144-1
 : Sequence 1, Application US/10270144
 : Publication No. US20030049790A1

GENERAL INFORMATION:

APPLICANT: MET, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

FILE REFERENCE: C100075000N

CURRENT APPLICATION NUMBER: US/10/270,144

CURRENT FILING DATE: 2002-10-15

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1014

TYPE: DNA

ORGANISM: Human

US-10-270-144-1

Alignment Scores:

Pred. No.: 1.5e-158 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775B-2 (1-337) x US-10-270-144-1 (1-1014)

QY 1 MetLsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 1 ATGATAGGCGACCTAGCATTTATAGCAATGCTTCTGATTTCCCGATATAGCATGCT 60
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTTCGAATTCAGTGTGATGATATGCGCTTACGCTTCATTCACCTGATATAGCAGC 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTTACTCTCCGCGGGATTTCCAGGCAATGCAATGATGATGATGATGATGATGAT 180
 QY 61 LysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGAGAGACGACACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyAsnTrrPle 100
 DB 241 CTGATCTGACGACCTTCCTCTCGATTCATCTACTATGCGAAGGGGAAACCTGGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTTCGAGATTCAGTGTGATGATATGCGCTTACGCTTCATTCACCTGATATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
 DB 361 ATTCCTCTCTCCACTGTTTCAGCATTTTCCTGCTACTGTCATTCACCATGAGC 420
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaCysAlaValIleTrrPleIle 160
 DB 421 TGCCTTTCATTCACAAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCATGTCGATGCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

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QY	21	PheGlyAsn	CysThrAsp	GluAsn	LeuPro	LeuIleu	SerMet	HisTyr	LeuPro	ValIle	Tyr	40	
Db	61	TTTGGAAAT	TGCAC	TGATG	AAAAACAT	TCCACAT	CAGAT	GACAT	CACTCC	CGTAT	TTAT	120	
QY	41	GlyIle	IlePhe	LeuVal	GlyPhe	ProGly	ValAsn	IleVal	Ile	SerThr	TyrIle	Phe	60
Db	121	GGCAT	TATCT	CTCTG	TGGAT	TTCAG	GCAAT	GAGAT	GATGAT	CAAT	CACTT	CAAT	180
QY	61	LysMet	IlePro	TyrPhe	SerSer	ThrIle	IleMet	LeuAsn	Ileu	Ileu	AspThr	AspLeu	80
Db	181	AAATG	AGAC	CTTGA	AGAC	GACAC	ACAT	TATTT	AGCTG	AAAC	CTGGC	CTGAC	240
QY	81	LeuTyr	LeuThr	SerLeu	ProPhe	LeuIle	HisTyr	TyrAla	SerGly	GluAsn	TyrPhe	100	
Db	241	CTTAT	CTATCA	CCAGC	CTCCCT	CTCTG	TATCA	CTATG	CAATG	CAATG	CGAAAACT	GGATC	300
QY	101	PheGly	AspPhe	MetCys	LysPhe	IleArg	PheSer	PheHis	AspAsn	LeuTyr	SerSer	120	
Db	301	TTTGG	AGAT	TTCAT	GATG	TATTT	ATTCG	CGCTT	CACTT	CAAC	CTGTAT	AGAC	360
QY	121	IleLeu	PheLeu	ThrCys	PheSer	IlePhe	ArgTyr	CysVal	IleIle	HisPhe	MetSer	140	
Db	361	ATCCT	TTCTG	CPAC	CGTTT	CAGC	ATCTT	CCGCA	CTGAT	GATG	CAAT	CAAT	420
QY	141	CysPhe	SerIle	HisLys	ThrArg	GlySala	IleVal	IleVal	IleAsp	Sala	IleVal	TyrPhe	160
Db	421	TGCTT	TTCAT	TCA	CAAA	AACTG	ATG	TCG	CAAT	TGTAG	CTGTG	CTGGT	480
QY	161	SerLeu	ValAla	ValIle	ProMet	ThrPhe	LeuIle	ThrSer	ThrAsn	ArgThr	AsnArg	180	
Db	481	TCCTG	TGTAG	CTG	TAT	TCCAT	CAATG	CACTT	TGTAT	CAATCA	ATCAAC	CAAG	540

Qy	181	SeRAlAcysLeuAspLeuThrSerSerSerSpGluLeuAsnThrIleLysTPTrpYAsnLeu	2000
Db	541	TCAGCCGTCTCGACCTCCACCAAGTGGATGACCATCACTATTAAAGTGTACAACTCG	6000
Qy	201	IleLeuThrAlaThrThpPheCysLeuProLeuValIleValIThrLysCysTyrThrThr	2200
Db	601	ATTTTACGCAACTACTTCTGCTCCCTCCCTGGGATAGGACACTTGGCTATACCAAG	6600
Qy	221	IleIleHisThrLeuThrHisGlyLeuGlnIlnHisAspSerCysLeuLysGlnLysAlaArg	2400
Db	661	ATTATTCACACACTCTGACCCATGGATCGCAAACTGCAAGCTGCTTAAAGCAAAAGCAAG	7200
Qy	241	ArgLeuThrIleLeuLeuLeuLeuAlaIlePheTyrValCysPheLeuProPheHisIleLeu	2600
Db	721	AGGCTAACCATTCCTGCTACTCTCTGCATTTCACGATGATTTTAACTCCCTGCATATCTTG	7800
Qy	261	ArgValIleArgIleGlnSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle	2800
Db	781	AGGCTCATTCGGATCGCAATCTGCCTGCTTCATCAATGATCTTCTCAATGAGAAATCAATC	8400
Qy	281	HisGlnAlaTyrTleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu	3000
Db	841	CATGAAAGCTTACATCGTTCTTGACCACTTAACTGCTCGAACACCTTCTGGCAACCTGTA	9000
Qy	301	LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValValArgCysLys	3200

QY	321	ValSerGlyAsnLeuGluGlnAlaIysIleSerTyrSerAsnAsnPro	337
DB	961	GTAGCGGGACCTTGACGACCAAGAAATAATGTTACTCAACACACCCCT	1011

Publication No. US20030088080A1
GENERAL INFORMATION:
APPLICANT: Communi, Didier
TITLE OF INVENTION: RECEPTOR GPCR-X10
FILE REFERENCE: 9409/2082

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Db 121 GGCAATATCTCTCTGTTGGATTTCCAGGCAATGCAATGATGATATTCACCTTACATTTTC 180
Qy 181 AAAATGAGACCTTGGAGAGACGACATCATTAATGGAACCTGGCTGACGATCTG 240
Db 181 AAAATGAGACCTTGGAGAGACGACATCATTAATGGAACCTGGCTGACGATCTG 240
Qy 241 CTGTATCTGACAGACCTCCCTCTGATGATGATGATGATGATGATGATGATGATG 300
Db 241 CTGTATCTGACAGACCTCCCTCTGATGATGATGATGATGATGATGATGATGATG 300
Qy 301 TTGGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 301 TTGGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 361 ATCCCTCTCTGACCTTTCAGCATCTTCGCTGATGATGATGATGATGATGATGATG 420
Db 361 ATCCCTCTCTGACCTTTCAGCATCTTCGCTGATGATGATGATGATGATGATGATG 420
Qy 421 TGGCTTTCCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATG 480
Db 421 TGGCTTTCCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATG 480
Qy 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy 541 TCAGCCGTCTGACCTGACATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 TCAGCCGTCTGACCTGACATGATGATGATGATGATGATGATGATGATGATGATG 600
Qy 601 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 660
Db 601 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 660
Qy 661 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
Db 661 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
Qy 721 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Qy 781 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy 841 CATGAAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 CATGAAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Qy 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Qy 961 GTAAAGCGGAACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
Db 961 GTAAAGCGGAACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014

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RESULT 2
US-10-270-144-1
; Sequence 1, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C10007500CN
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-1
Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 8e-301;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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please note that it's 100% actually!

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Qy 1 ATGAATGAGACCTAGACATTAATGCAAAATGCTTCTGATTTCCCGATATGAGAGCTG 60
Db 1 ATGAATGAGACCTAGACATTAATGCAAAATGCTTCTGATTTCCCGATATGAGAGCTG 60
Qy 61 TTGGAAATTTGCACTGATGAAATATCCACCTGATGATGATGATGATGATGATGATG 120
Db 61 TTGGAAATTTGCACTGATGAAATATCCACCTGATGATGATGATGATGATGATGATG 120
Qy 121 GGCAATATCTCTCTGTTGGATTTCCAGGCAATGCAATGATGATGATGATGATGATG 180
Db 121 GGCAATATCTCTCTGTTGGATTTCCAGGCAATGCAATGATGATGATGATGATGATG 180
Qy 181 AAAATGAGACCTTGGAGAGACGACATCATTAATGGAACCTGGCTGACGATCTG 240
Db 181 AAAATGAGACCTTGGAGAGACGACATCATTAATGGAACCTGGCTGACGATCTG 240
Qy 241 CTGTATCTGACAGACCTCCCTCTGATGATGATGATGATGATGATGATGATGATGATG 300
Db 241 CTGTATCTGACAGACCTCCCTCTGATGATGATGATGATGATGATGATGATGATGATG 300
Qy 301 TTGGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 301 TTGGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 361 ATCCCTCTCTGACCTTTCAGCATCTTCGCTGATGATGATGATGATGATGATGATG 420
Db 361 ATCCCTCTCTGACCTTTCAGCATCTTCGCTGATGATGATGATGATGATGATGATG 420
Qy 421 TGGCTTTCCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATGATG 480
Db 421 TGGCTTTCCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATGATG 480
Qy 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy 541 TCAGCCGTCTGACCTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Db 541 TCAGCCGTCTGACCTGACATGATGATGATGATGATGATGATGATGATGATGATGATG 600
Qy 601 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 660
Db 601 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 660
Qy 661 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
Db 661 ATTTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
Qy 721 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Qy 781 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 AGGCTAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy 841 CATGAAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 CATGAAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Qy 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960

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Db 901 CTATATGCTGCTGAGGAGCAACTTTCAGCAGGCTGCTGCTCAACAGCTGAGATGCAAA 960
 Oy 961 GTAACGGGAACCTTGAGCAGCAAGAAATTAAGTACTCAACAAACCTTGA 1014
 Db 961 GTAACGGGAACCTTGAGCAGCAAGAAATTAAGTACTCAACAAACCTTGA 1014

RESULT 3

US-10-188-405-7

Sequence 7, Application US/10188405
 Publication No. US20030082585A1
 GENERAL INFORMATION:
 APPLICANT: Tian, Hui
 APPLICANT: Dai, Kang
 APPLICANT: Chen, Jin-Long
 APPLICANT: Zhao, Jiagang
 APPLICANT: Cutler, Gene
 APPLICANT: Tularik Inc.
 TITLE OF INVENTION: No. US20030082585A1el Receptors
 FILE REFERENCE: 018781-008410US
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: US 60/302,800
 PRIOR FILING DATE: 2001-07-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 7
 LENGTH: 1014
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human TGR164
 US-10-188-405-7

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 8e-301; Indels 0; Gaps 0;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ATGAATGAGCAGCACTAGACATATTAGCAAAATGCTTCTGATTTCCCGATTATGAGCTGCT 60
 Db 1 ATGAATGAGCAGCACTAGACATATTAGCAAAATGCTTCTGATTTCCCGATTATGAGCTGCT 60
 Oy 61 TTTGAAAATGACATGATGATAAATACCCACATCAAGATGACATGACTGCTGATTTAT 120
 Db 61 TTTGAAAATGACATGATGATAAATACCCACATCAAGATGACATGACTGCTGATTTAT 120
 Oy 121 GGCATTATCTCTGCTGAGGATTTCCAGCAATGAGATGATATCCACTTACATTTTC 180
 Db 121 GGCATTATCTCTGCTGAGGATTTCCAGCAATGAGATGATATCCACTTACATTTTC 180
 Oy 181 AAAATGAGACCTTGAAGAGAGACACCAATCATTTATGCTGAACCTGCGCTGCACAGATCTG 240
 Db 181 AAAATGAGACCTTGAAGAGAGACACCAATCATTTATGCTGAACCTGCGCTGCACAGATCTG 240
 Oy 241 CTGTATCTGACAGCTCCCTTCTGATTTCACTATATGAGAGTGGCAAAATCTGATC 300
 Db 241 CTGTATCTGACAGCTCCCTTCTGATTTCACTATATGAGAGTGGCAAAATCTGATC 300
 Oy 301 TTTGAGATTTTCATGTAGTAAATTTATCCGCTTCACTGCTCAATTTCAACCTGATATGACAG 360
 Db 301 TTTGAGATTTTCATGTAGTAAATTTATCCGCTTCACTGCTCAATTTCAACCTGATATGACAG 360
 Oy 361 ATCTCTTCTCAGCTGTTTACAGCATCTCCGCTACTGCTGATGATCTTCAACCAATGAGC 420
 Db 361 ATCTCTTCTCAGCTGTTTACAGCATCTCCGCTACTGCTGATGATGATCAACCAATGAGC 420
 Oy 421 TCGTTTTCATTCACAAACTGATGTGAGTTGAGCTGCTGCTGATGATGATTTAT 480
 Db 421 TCGTTTTCATTCACAAACTGATGTGAGTTGAGCTGCTGCTGATGATGATTTAT 480
 Oy 481 TCACGTGAGCTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 481 TCACGTGAGCTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

Db 481 TCACGTGAGCTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Oy 541 TCAGCTGCTGCTGAGCTTACACAGTTGCGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 541 TCAGCTGCTGCTGAGCTTACACAGTTGCGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Oy 601 ATTTGACTGCACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 601 ATTTGACTGCACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Oy 661 ATTATTCACACTCTGACCCATGACTGCAAAATGACAGCTGCTTATGAGAGAGACAGCA 720
 Db 661 ATTATTCACACTCTGACCCATGACTGCAAAATGACAGCTGCTTATGAGAGAGAGACAGCA 720
 Oy 721 AGGCTACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Db 721 AGGCTACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 Oy 781 AGGCTACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 781 AGGCTACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Oy 841 CATGAAGCTTACATGCTTCTGACCATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 841 CATGAAGCTTACATGCTTCTGACCATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Oy 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Db 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Oy 961 GTAACGGGAACCTTGAGCAGCAAGAAATTAAGTACTCAACAAACCTTGA 1014
 Db 961 GTAACGGGAACCTTGAGCAGCAAGAAATTAAGTACTCAACAAACCTTGA 1014

RESULT 4

US-09-885-453-2

Sequence 2, Application US/09885453
 Publication No. US2003008080A1
 GENERAL INFORMATION:
 APPLICANT: Communi, Didier
 TITLE OF INVENTION: RECEPTOR GPCR10
 FILE REFERENCE: 9409/2082
 CURRENT APPLICATION NUMBER: US/09/885,453
 CURRENT FILING DATE: 2001-06-20
 PRIOR APPLICATION NUMBER: US 09/885,453
 PRIOR FILING DATE: 2001-06-21
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patent In version 3.1
 SEQ ID NO 2
 LENGTH: 1014
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: DNA nucleotide sequence
 LOCATION: (1)..(1014)
 OTHER INFORMATION: GPCR10 DNA sequence
 US-09-885-453-2

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 8e-301; Indels 0; Gaps 0;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ATGAATGAGCAGCACTAGACATATTAGCAAAATGCTTCTGATTTCCCGATTATGAGCTGCT 60
 Db 1 ATGAATGAGCAGCACTAGACATATTAGCAAAATGCTTCTGATTTCCCGATTATGAGCTGCT 60
 Oy 61 TTTGAAAATGACATGATGATAAATACCCACATCAAGATGACATGACTGCTGATTTAT 120
 Db 61 TTTGAAAATGACATGATGATAAATACCCACATCAAGATGACATGACTGCTGATTTAT 120
 Oy 121 GGCATTATCTCTGCTGAGGATTTCCAGCAATGAGATGATATCCACTTACATTTTC 180
 Db 121 GGCATTATCTCTGCTGAGGATTTCCAGCAATGAGATGATATCCACTTACATTTTC 180

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Db 121 ILFLGCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Qy 181 SACLDTSSDELNTIKMYNLIATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKMYNLIATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISCIENQIHEAVIYSRPLAALNTFGNL 300
Db 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISCIENQIHEAVIYSRPLAALNTFGNL 300
Qy 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337
Db 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337

RESULT 2

US-10-270-144-2
; Sequence 2, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Human
US-10-270-144-2

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3 2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Db 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Qy 61 KMRPKSSITIMINACTDLIYLSPLPHIHYASGNNIFGDMCKFRFSHFNLXS 120
Db 61 KMRPKSSITIMINACTDLIYLSPLPHIHYASGNNIFGDMCKFRFSHFNLXS 120
Qy 121 ILFLGCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Db 121 ILFLGCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Qy 181 SACLDTSSDELNTIKMYNLIATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKMYNLIATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISCIENQIHEAVIYSRPLAALNTFGNL 300
Db 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISCIENQIHEAVIYSRPLAALNTFGNL 300
Qy 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337
Db 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337

RESULT 3

US-10-188-405-8
; Sequence 8, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long
APPLICANT: Zhao, Jiagang
APPLICANT: Cutler, Gene
APPLICANT: Tularix Inc.
; TITLE OF INVENTION: NO. US20030082585A1 Receptors
; FILE REFERENCE: 018781-00841005
; CURRENT APPLICATION NUMBER: US/10/188,405
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR164
US-10-188-405-8

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3 2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Db 1 MNEPLDYLANASDPDYAAAFGNCCTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Qy 61 KMRPKSSITIMINACTDLIYLSPLPHIHYASGNNIFGDMCKFRFSHFNLXS 120
Db 61 KMRPKSSITIMINACTDLIYLSPLPHIHYASGNNIFGDMCKFRFSHFNLXS 120
Qy 121 ILFLGCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Db 121 ILFLGCSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Qy 181 SACLDTSSDELNTIKMYNLIATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKMYNLIATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISCIENQIHEAVIYSRPLAALNTFGNL 300
Db 241 RLTIILLAFYVCFPLPHILRVIRIESRLISCSISCIENQIHEAVIYSRPLAALNTFGNL 300
Qy 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337
Db 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337

RESULT 4

US-09-885-453-1
; Sequence 1, Application US/09885453
; Publication No. US2003008080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCR10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: amino acid sequence GPCR10
; LOCATION: (1)-(337)
; OTHER INFORMATION: GPCR10 amino acid sequence
US-09-885-453-1

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RS Claim 2; Page 30; 37pp; English.

CC The invention relates to an isolated AXOR89 polypeptide (G-protein
CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
CC and polynucleotide encoding the polypeptide, is useful for identifying
CC agonists and antagonists (or inhibitors) that are potentially useful in
CC treating conditions associated with an AXOR89 imbalance, such as
CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
CC Parkinson's Disease, diabetes, obesity, anorexia, bulimia, acute heart
CC failure, hypertension, hyperextension, urinary retention, osteoporosis,
CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
CC syndrome. The polynucleotide sequence may also be used for chromosome
CC localization or tissue expression studies. The AXOR89 is used as a
CC vaccine or to produce fusion proteins. The present sequence is human
CC AXOR89 cDNA.

XX Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match 100.0%; Score 1014; DB 24; Length 1014;
Best Local Similarity 100.0%; Pred. No. 7, 1e-289;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAATGAGCCACTACACTATTTAGCAATGCTTGTGATTTCCCGATTGACAGCTGCT 60
DB 1 ATGAAATGAGCCACTACACTATTTAGCAATGCTTGTGATTTCCCGATTGACAGCTGCT 60
QY 61 TTGGAAATGAGCCACTACACTATTTAGCAATGCTTGTGATTTCCCGATTGACAGCTGCT 120
DB 61 TTGGAAATGAGCCACTACACTATTTAGCAATGCTTGTGATTTCCCGATTGACAGCTGCT 120
QY 121 GGCATATCTCTCCCTGGGATTTCCAGGAAATGCTAGTATGATTCACCTATTTTC 180
DB 121 GGCATATCTCTCCCTGGGATTTCCAGGAAATGCTAGTATGATTCACCTATTTTC 180
QY 181 AAAATGAGACTTGGAGAGAGACACCATCATTTATGCTGAACTGGCTGACACAGATCG 240
DB 181 AAAATGAGACTTGGAGAGAGACACCATCATTTATGCTGAACTGGCTGACACAGATCG 240
QY 241 CTGTATCTGACGCGCTCCCTCCCTGATTCATCTATGCTGAGTGGCGAAATGATG 300
DB 241 CTGTATCTGACGCGCTCCCTCCCTGATTCATCTATGCTGAGTGGCGAAATGATG 300
QY 301 TTGGAGATTTTCATGTAAGTTATCCGCTCAGCTTCATTTTAACTGTATAGCAGC 360
DB 301 TTGGAGATTTTCATGTAAGTTATCCGCTCAGCTTCATTTTAACTGTATAGCAGC 360
QY 361 ATCCCTCTCTCAGCTGTTTACAGCATCTTCCGCTACTGTGTATCATTTACCAATGAGC 420
DB 361 ATCCCTCTCTCAGCTGTTTACAGCATCTTCCGCTACTGTGTATCATTTACCAATGAGC 420
QY 421 TGGTTTTCATTTACAAAATCGATGTGAGTGTGAGTGTGCTGTGTGTGATATTT 480
DB 421 TGGTTTTCATTTACAAAATCGATGTGAGTGTGAGTGTGCTGTGTGTGATATTT 480
QY 481 TCACGTGATGCTGATTCGATGAGTACCTTGTGATGATCAACCAAGAGACAGCA 540
DB 481 TCACGTGATGCTGATTCGATGAGTACCTTGTGATGATCAACCAAGAGACAGCA 540
QY 541 TCAGCTGCTGCTGAGCTGACACATGCGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TCAGCTGCTGCTGAGCTGACACATGCGATGATGATGATGATGATGATGATGATGAT 600
QY 601 ATTTGACATGCACTATTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 ATTTGACATGCACTATTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 ATTTGACATGCACTATTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 ATTTGACATGCACTATTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 721 AGGCTAACCATCTGCTACTCCCTGCAATTTAGATGTTTATACCTTCATATCTG 780
DB 721 AGGCTAACCATCTGCTACTCCCTGCAATTTAGATGTTTATACCTTCATATCTG 780
QY 781 AGGCTAACCATCTGCTACTCCCTGCAATTTAGATGTTTATACCTTCATATCTG 840
DB 781 AGGCTAACCATCTGCTACTCCCTGCAATTTAGATGTTTATACCTTCATATCTG 840
QY 841 CATGAAGCTTACATCTTTCTGAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 CATGAAGCTTACATCTTTCTGAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 CTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GTAAGCGGAGACCTTACAGCAAGCAAAATTTAGTACTGCAACCACTTGA 1014
DB 961 GTAAGCGGAGACCTTACAGCAAGCAAAATTTAGTACTGCAACCACTTGA 1014

RESULT 3

AAD26370
ID AAD26370 standard; cDNA; 1014 BP.

XX AAD26370;

DE 26-MAR-2002 (first entry)

XX Human G-protein coupled receptor 2 (GRC-2) cDNA.

XX Human; G-protein coupled receptor 2; cell proliferative disorder;
XX arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
XX atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
XX gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
XX acquired immune deficiency syndrome; inflammatory disorder; infection;
XX Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
XX diabetes; obesity; osteoporosis; gene therapy; GRC-2; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1014

FT /tag-a

FT /product- "Human GRC-2 protein"

PN WO200187937-A2.

PD 22-NOV-2001.

PE 17-MAY-2001; 2001MO-US16285.

PR 18-MAY-2000; 2000US-205628P.

PR 22-MAY-2000; 2000US-206222P.

PR 25-MAY-2000; 2000US-207566P.

PR 02-JUN-2000; 2000US-208834P.

PR 02-JUN-2000; 2000US-208861P.

PA (INCY-) INCYTE GENOMICS INC.

PI Patterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R;

PI Khan FA, Gandhi AR, Wajia NR, Nguyen DB, Yue H, Hafalia A;

PI Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;

XX MPI; 2002-089844/12.

XX P-PSDB; AAE16171.

XX Novel G-protein coupled receptors and polynucleotides useful for

PT diagnosis, treatment and prevention of disorders of cell proliferation,

PT neurological, cardiovascular, metabolic disorders and viral infections

PT

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PS Claim 5; Page 111-112; 115pp; English.

XX The invention relates to human G-protein coupled receptor (GCRG)

CC polypeptides and polynucleotides. GCRG polypeptides are useful for

CC screening compounds that modulate their activity. They are useful in

CC the diagnosis, prevention and treatment of disorders which include

CC cell proliferative disorders such as arteriosclerosis, hepatitis,

CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukemia,

CC lymphoma; neurological disorders such as epilepsy, ischemic

CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,

CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral

CC meningitis, Creutzfeldt-Jakob disease, schizophrenia disorders, amnesia;

CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,

CC hypertension, vascular tumours, myocardial infarction, hypertensive

CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;

CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,

CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,

CC constipation, acquired immune deficiency syndrome (AIDS), hepatic

CC encephalopathy; autoimmune/inflammatory disorders such as Addison's

CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact

CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,

CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid

CC arthritis, systemic lupus erythematosus, warts, viral, bacterial,

CC fungal, parasitic, protozoal and helminthic infections and trauma;

CC metabolic disorders such as diabetes, obesity and osteoporosis; and

CC viral infections such as infection caused by viral agent classified as

CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention

CC are useful as probes for assessing toxicity of test compounds. They are

CC also used in gene therapy. The present sequence is human G-protein

CC coupled receptor 2 (GCRG-2) cDNA.

XX

XX Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match 100.0%; Score 1014; DB 24; Length 1014;

Best Local Similarity 100.0%; Pred. No. 7.1e-289;

Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGCCAGTACATTTAGCAATGCTTCTGATTTCCCGATTATGACAGCTCT 60

DB 1 ATGATGAGCCAGTACATTTAGCAATGCTTCTGATTTCCCGATTATGACAGCTCT 60

QY 61 TTGGAAATTCACATGATGAAACATCCACATCAAGATGACACTACCTCTGTTATTTAT 120

DB 61 TTGGAAATTCACATGATGAAACATCCACATCAAGATGACACTACCTCTGTTATTTAT 120

QY 121 GGCATTTCTCTCTGCTGGGATTTCCAGCAATGCAATGATGATATTCACATTTATTC 180

DB 121 GGCATTTCTCTCTGCTGGGATTTCCAGCAATGCAATGATGATATTCACATTTATTC 180

QY 181 AAATGAGACCTGGAAAGAGAGACGACATCAATGATGCAAGCCCTGCAAGATG 240

DB 181 AAATGAGACCTGGAAAGAGAGACGACATCAATGATGCAAGCCCTGCAAGATG 240

QY 241 CTGATCTGACAGCTCCCTCTCTGATTCATCTATGACAGTGGGAAATGATG 300

DB 241 CTGATCTGACAGCTCCCTCTCTGATTCATCTATGACAGTGGGAAATGATG 300

QY 301 TTGGAGATTTTCATGTTAGTTATCCGCTTCACCTTCACCTTCACCTGTTATGACAG 360

DB 301 TTGGAGATTTTCATGTTAGTTATCCGCTTCACCTTCACCTTCACCTGTTATGACAG 360

QY 361 ATTCCTTCCTCAGCTGTTTACGATCTTCCGCTCTGATGATGATGATGATGATG 420

DB 361 ATTCCTTCCTCAGCTGTTTACGATCTTCCGCTCTGATGATGATGATGATGATG 420

QY 421 TGCTTTTCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATG 480

DB 421 TGCTTTTCATTCACAAACTGATGATGATGATGATGATGATGATGATGATGATG 480

QY 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

DB 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

QY 541 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600

DB 541 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 601 ATTTGACCTGCAACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

DB 601 ATTTGACCTGCAACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 661 ATTTGACCTGCAACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

DB 661 ATTTGACCTGCAACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

QY 721 AGGCTACATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

DB 721 AGGCTACATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 781 AGGCTACATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

DB 781 AGGCTACATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 841 CAGTACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

DB 841 CAGTACCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

QY 961 GTAAAGCGGAACTTGGAGCAAGCAAAATTTGTTTCTGCAAAACCACTTGA 1014

DB 961 GTAAAGCGGAACTTGGAGCAAGCAAAATTTGTTTCTGCAAAACCACTTGA 1014

RESULT 4

AA507948

ID AA507948 standard; cDNA; 1014 BP.

XX AA507948;

XX 23-OCT-2001 (first entry)

XX Human cDNA encoding G-protein coupled receptor, hRUP21.

XX Human G-protein coupled receptor; GPCR; hRUP21; agonist;

XX Inverse agonist; lung cancer; ss.

XX Homo sapiens.

XX OS

XX Key

FT CDS

FT 1.1014

FT Location/Qualifiers

FT /product="hRUP21"

PN WO200136471-A2.

PD 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US31509.

PF 17-NOV-1999; 99US-0166088.

PR 17-NOV-1999; 99US-0166099.

PR 17-NOV-1999; 99US-0166369.

PR 23-DEC-1999; 99US-0171900.

PR 23-DEC-1999; 99US-0171901.

PR 23-DEC-1999; 99US-0171902.

PR 11-FEB-2000; 2000US-0181749.

PR 14-MAR-2000; 2000US-0189258.

PR 14-MAR-2000; 2000US-0189259.

PR 10-APR-2000; 2000US-0195898.

PR 10-APR-2000; 2000US-0195899.

PR 10-APR-2000; 2000US-0196078.

PR 28-APR-2000; 2000US-0200419.

PR 12-MAY-2000; 2000US-0203630.

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DR P-PSDB; ABB83819.
 XX An isolated P2Y₁-like receptor polypeptide (HIPHM 000037) which can be
 PT used for the identification of agonists and antagonists which may be
 PS used to treat an immune or inflammatory disease -
 XX Claim 5; Page 28-29; 35pp; English.
 XX The invention relates to an isolated P2Y₁-like receptor polypeptide
 CC (ABB83818-ABB83819) which is also referred to in the specification as
 CC HIPHM 000037. An effective amount of a substance (agonist or
 CC antagonist) which modulates P2Y₁ receptor activity is useful to treat a
 CC subject having a disorder that is responsive to P2Y₁-like receptor
 CC modulation. The disorder is a disease of immunity or inflammation. The
 CC substance may also be used to manufacture a medicine for the treatment or
 CC prophylaxis of a disorder that is responsive to stimulation or modulation
 CC of P2Y₁-like receptor activity. Disorders which may be treated include
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
 CC polyarthritis or prostaticitis. The invention provides alternative
 CC substances for the treatment of immunological and inflammatory diseases.
 CC The present sequence is that the P2Y₁-like receptor variant encoding gene
 CC of the invention.
 XX
 SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other:

Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACCTAGACTATTTAGCAATGCTTGTATTTCCCGATTATGACCTGCT 60
 DB 1 ATGATGAGCCACCTAGACTATTTAGCAATGCTTGTATTTCCCGATTATGACCTGCT 60
 QY 61 TTGGAAATTCACCTGATGAAACATCCACCTCAAGAGACCTACCTCCCTGTTATTTAT 120
 DB 61 TTGGAAATTCACCTGATGAAACATCCACCTCAAGAGACCTACCTCCCTGTTATTTAT 120
 QY 121 GGCAATATCTTCCTGCGGAGTTTCCAGCAATGAGTAGATATCCACTTATTTTC 180
 DB 121 GGCAATATCTTCCTGCGGAGTTTCCAGCAATGAGTAGATATCCACTTATTTTC 180
 QY 181 AAAATGAGACCTTGGAGAGACGACCATATTAATGCTGAGACCTGCTGCACAGATCTG 240
 DB 181 AAAATGAGACCTTGGAGAGACGACCATATTAATGCTGAGACCTGCTGCACAGATCTG 240
 QY 241 CTGATCTGACAGCCTCCCTCTCTGATTCCTATTCGCAAGTGGGAAACCTGATC 300
 DB 241 CTGATCTGACAGCCTCCCTCTCTGATTCCTATTCGCAAGTGGGAAACCTGATC 300
 QY 301 TTGGAGATTCATGATGATTAATTCGCTTCACTTCCATTTCAACCTGATATGACG 360
 DB 301 TTGGAGATTCATGATGATTAATTCGCTTCACTTCCATTTCAACCTGATATGACG 360
 QY 361 ATTCCTCTCTACCTGTTTACGATCTTCGCTACTGTGATATTCACCAATGAGC 420
 DB 361 ATTCCTCTCTACCTGTTTACGATCTTCGCTACTGTGATATTCACCAATGAGC 420
 QY 421 TGCCTTTCATTCACAAAACGATGAGTGAAGTGGAGCTGGGTGGTGGATTCAT 480
 DB 421 TGCCTTTCATTCACAAAACGATGAGTGAAGTGGAGCTGGGTGGTGGATTCAT 480
 QY 481 TCACGTGATGCTGATTCGATGACCTTCTGATCACAATCAACAGACCAACGA 540
 DB 481 TCACGTGATGCTGATTCGATGACCTTCTGATCACAATCAACAGACCAACGA 540
 QY 541 TCAGCCTGCTGACCTCAACAGTTCGATGAGTGAATCAATATTAAGTGGTGAACCTTA 600
 DB 541 TCAGCCTGCTGACCTCAACAGTTCGATGAGTGAATCAATATTAAGTGGTGAACCTTA 600

QY 601 ATTTGACAGCAACTACTTTCCTCCCTTGGTGTATGATGACACTTTCCTATACACG 660
 DB 601 ATTTGACAGCAACTACTTTCCTCCCTTGGTGTATGATGACACTTTCCTATACACG 660
 QY 661 ATATTCACACCTGACCCCATGAGACGCAACGACGCTGCTTAAGCAAGACGCA 720
 DB 661 ATATTCACACCTGACCCCATGAGACGCAACGACGCTGCTTAAGCAAGACGCA 720
 QY 721 AGGCTACATTCCTGACCTGCTTGCATTTAGATGTTTATACCTTCATATCTTG 780
 DB 721 AGGCTACATTCCTGACCTGCTTGCATTTAGATGTTTATACCTTCATATCTTG 780
 QY 781 AGGCTACATTCCTGACCTGCTTGCATTTAGATGTTTATACCTTCATATCTTG 840
 DB 781 AGGCTACATTCCTGACCTGCTTGCATTTAGATGTTTATACCTTCATATCTTG 840
 QY 841 CATGACCTTACATCTGTTTATACCTTATGCTGCTGTAACACCTTGTGAACCTTGA 900
 DB 841 CATGACCTTACATCTGTTTATACCTTATGCTGCTGTAACACCTTGTGAACCTTGA 900
 QY 901 CTATATGCTGCTGACGACGACCACTTTCACAGAGCTGCTGCTCAACAGTGAATGCA 960
 DB 901 CTATATGCTGCTGACGACGACCACTTTCACAGAGCTGCTGCTCAACAGTGAATGCA 960
 QY 961 GTAAGCGGAACTTGGAGCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTA 1014
 DB 961 GTAAGCGGAACTTGGAGCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTA 1014

RESULT 6
 ABRK1381
 ID ABRK1381 standard; DNA; 1014 BP.

ABK1381;
 05-JUN-2002 (first entry)
 Human DNA encoding P2Y₁-like G protein-coupled receptor.

Human: ds; gene; P2Y₁-like G-protein-coupled receptor; GPCR;
 infection; pain; cancer; anorexia; bulimia; asthma; hypotension;
 central nervous system disease; acute heart failure; hypertension;
 urinary retention; osteoporosis; diabetes; angina pectoris;
 myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 benign prostatic hyperplasia; psychosis; neurological disorder;
 dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
 Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 dementia; severe mental retardation; Huntington's disease;
 Tourette's syndrome.

Homo sapiens.
 Key Location/Qualifiers
 CDS 1..1014
 FT /*tag= a
 FT /product= "P2Y₁-like GPCR"

W0200214511-A2.
 21-FEB-2002.
 10-AUG-2001; 2001WO-EP09243.
 14-AUG-2000; 2000US-224989P.
 (FARB) BAYER AG.
 Ramakrishnan S;
 WPI; 2002-257607/30.
 DR P-PSDB; AAU77600.
 XX Novel human P2Y₁-like G protein-coupled receptor polypeptide which can

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PT be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 XX
 PS Claim 1: Fig 5, 118pp: English.

XX The invention relates to a purified human P2Y1-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y1-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence encodes the P2Y1-like GPCR of the invention.
 XX
 XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2,1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTAGACTATTAGCAAAATGCTTCGATTCCCGCATATGACAGCTGCT 60
 DB 1 ATGATGAGCCACTAGACTATTAGCAAAATGCTTCGATTCCCGCATATGACAGCTGCT 60
 QY 61 TTGGAAATTTGCACTATGAAAAATCCCAAGATGACATCTCCCTGTTATTTAT 120
 DB 61 TTGGAAATTTGCACTATGAAAAATCCCAAGATGACATCTCCCTGTTATTTAT 120
 QY 121 GGCATATCTCTCTGCGGATTTCCAGGATGACATGATGATGATGATGATGATGATGAT 180
 DB 121 GGCATATCTCTCTGCGGATTTCCAGGATGACATGATGATGATGATGATGATGATGAT 180
 QY 181 AAAATGAGACCTTGAAGAGACACACATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
 DB 181 AAAATGAGACCTTGAAGAGACACACATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
 QY 241 CTGTATCTGACAGCCTCCCTCTCGATTCACATCTAGTCCAGTGGCGAAAATGATGATC 300
 DB 241 CTGTATCTGACAGCCTCCCTCTCGATTCACATCTAGTCCAGTGGCGAAAATGATGATC 300
 QY 301 TTGGAGATTTATGTAAGTATATCCGCTGAGCTTCATTTCAACCTGATATGAGAGC 360
 DB 301 TTGGAGATTTATGTAAGTATATCCGCTGAGCTTCATTTCAACCTGATATGAGAGC 360
 QY 361 ATCCCTCTCTCACTGTTTACAGATCTCCGCTAGCTGTGATGATTCACCAATGAGC 420
 DB 361 ATCCCTCTCTCACTGTTTACAGATCTCCGCTAGCTGTGATGATTCACCAATGAGC 420
 QY 421 TCGTTTTCATTCACAAAACCTGATGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGT 480
 DB 421 TCGTTTTCATTCACAAAACCTGATGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGT 480
 QY 481 TCACCTGTAGCTCTCATTCGATGAGCTTTTATGATCATCAACACAGAGACCAAGAGA 540
 DB 481 TCACCTGTAGCTCTCATTCGATGAGCTTTTATGATCATCAACACAGAGACCAAGAGA 540
 QY 541 TCAGCTGTCTGACCTCAACCACTGATGAGTGAATCAATCTATTAAGTGGTCAACCTGA 600
 DB 541 TCAGCTGTCTGACCTCAACCACTGATGAGTGAATCAATCTATTAAGTGGTCAACCTGA 600

QY 601 ATTATGACCTGCAACTCTTTCGCTCCCTCCCTGGTATGATGACATCTTGTATACAGC 660
 DB 601 ATTATGACCTGCAACTCTTTCGCTCCCTCCCTGGTATGATGACATCTTGTATACAGC 660
 QY 661 ATTATGACCTGCTGACACCTGATGACGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
 DB 661 ATTATGACCTGCTGACACCTGATGACGCAAACTGACAGCTGCTTAAAGCAGAAAGCAGA 720
 QY 721 AGGCTAACATCTCTGCTACTCTGCTGATTTTACGATGATGATGATGATGATGATGATGAT 780
 DB 721 AGGCTAACATCTCTGCTACTCTGCTGATTTTACGATGATGATGATGATGATGATGATGAT 780
 QY 781 AGGCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 AGGCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 CATGAGCTTACATCTCTTCTAGACCATTAGCTGCTGACACCTTTGGTAACTGTTA 900
 DB 841 CATGAGCTTACATCTCTTCTAGACCATTAGCTGCTGACACCTTTGGTAACTGTTA 900
 QY 901 CTATATGCTGTGTGTCAGCAGACACTTTTACAGAGCTGTCTGCTCAACAGTACATGCAAA 960
 DB 901 CTATATGCTGTGTGTCAGCAGACACTTTTACAGAGCTGTCTGCTCAACAGTACATGCAAA 960
 QY 961 GTAGGGGAGACCTTACAGCAGAAAGAAATTTAGTACTCAAAACACCTTGA 1014
 DB 961 GTAGGGGAGACCTTACAGCAGAAAGAAATTTAGTACTCAAAACACCTTGA 1014

RESULT 7
 AAK98323
 ID AAK98323 standard; cDNA; 1014 BP.
 AC AAK98323;
 AC AAK98323;
 DT 30-APR-2002 (first entry)
 XX
 DE Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.
 XX
 KW Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
 KW signal transduction; human protease; GPCR disorder; gene therapy;
 KW transgenic animal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag= a
 FT /product= "G-protein coupled receptor"
 PN WO200187980-A2.
 PN
 PD 22-NOV-2001.
 PD
 PE 17-MAY-2001; 2001MO-US15957.
 PE
 PR 18-MAY-2000; 2000US-205196P.
 PR 08-AUG-2000; 2000US-0634656.
 PR
 PA (APPL-) APPLERA CORP.
 PA
 XX Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
 PT WPI; 2002-075312/10.
 DR P-PSDB; AA014027.
 DR
 XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterised by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies
 PS Claim 23; Fig 1; 64pp: English.

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XX The present specifically claimed human cDNA sequence (located on
 CC chromosome 13) encodes a purinergic-related G-protein coupled receptor
 CC (GPCR) of the invention. GPCRs constitute a major class of proteins
 CC responsible for signal transduction within a cell. Upon binding of a
 CC ligand to the extracellular portion of a GPCR, a signal is transduced
 CC resulting in a biological or physiological change within the cell. The
 CC GPCR proteins can be divided into five families, family I contains the
 CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are
 CC characterised by their selective responsiveness towards ATP and its
 CC analogues, some also respond to UTP. The invention comprises a human
 CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR
 CC protein and nucleic acids of the invention are useful in the treatment of
 CC a disease or condition mediated by a human protease. The GPCR protein of
 CC the invention is useful for: the development/identification of
 CC therapeutic proteins; assays designed to quantitatively determine levels
 CC of the protein in biological fluids; identifying compounds which modulate
 CC the activity of the GPCR, or the interaction of the GPCR and a molecule
 CC with which it normally interacts; and treating a disorder characterised
 CC by an absence of, or inappropriate expression of the GPCR protein. The
 CC GPCR nucleic acids of the invention are useful in diagnostic assays to
 CC identify changes in the GPCR nucleic acid that lead to pathology.
 CC Controlling GPCR expression; and in gene therapy to treat patients with
 CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
 CC the production of transgenic animals.
 XX
 SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;
 Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 ATGATGAGCCACTAGACTATTAGCAATGCTTCGATTTCCCGCATATGAGCTGCT 60
 Db 1 ATGATGAGCCACTAGACTATTAGCAATGCTTCGATTTCCCGCATATGAGCTGCT 60
 Oy 61 TTTGGAAATGGACATGATGAAATGATCCACATGAGTGAATGAGTCCCTGTTATTTAT 120
 Db 61 TTTGGAAATGGACATGATGAAATGATCCACATGAGTGAATGAGTCCCTGTTATTTAT 120
 Oy 121 GGCATATATCTTCCTCGTGGGATTTCCAGGCAATGCAATGATGATTCATTTATTC 180
 Db 121 GGCATATATCTTCCTCGTGGGATTTCCAGGCAATGCAATGATGATTCATTTATTC 180
 Oy 181 AAAATGAGACCTTGGAGAGACGACACATCATATGCTGAACTGGCTGACAAAGATCTG 240
 Db 181 AAAATGAGACCTTGGAGAGACGACACATCATATGCTGAACTGGCTGACAAAGATCTG 240
 Oy 241 CTGTATCTGACGAGCTCCGCTTCGATTCATGATGAGTGGGCGAAATGAGATC 300
 Db 241 CTGTATCTGACGAGCTCCGCTTCGATTCATGATGAGTGGGCGAAATGAGATC 300
 Oy 301 TTTGAGATTTATGATGATGATTTATCCGCTTCAGTTCATTTCAACGATATAGAGC 360
 Db 301 TTTGAGATTTATGATGATGATTTATCCGCTTCAGTTCATTTCAACGATATAGAGC 360
 Oy 361 ATCCCTTCTCTACCTGTTTACAGATCTTCGCTACTGTTGATCATTCACCAAGAGC 420
 Db 361 ATCCCTTCTCTACCTGTTTACAGATCTTCGCTACTGTTGATCATTCACCAAGAGC 420
 Oy 421 ATCCCTTCTCTACCTGTTTACAGATCTTCGCTACTGTTGATCATTCACCAAGAGC 480
 Db 421 ATCCCTTCTCTACCTGTTTACAGATCTTCGCTACTGTTGATCATTCACCAAGAGC 480
 Oy 481 TCACCTGATGCTGATTCGATGAGCTTCGATGATCATTCACCAAGAGCAGACAGAG 540
 Db 481 TCACCTGATGCTGATTCGATGAGCTTCGATGATCATTCACCAAGAGCAGACAGAG 540
 Oy 541 TCACCTGATGCTGATTCGATGAGCTTCGATGATCATTCACCAAGAGCAGACAGAG 600
 Db 541 TCACCTGATGCTGATTCGATGAGCTTCGATGATCATTCACCAAGAGCAGACAGAG 600
 Oy 601 ATTTTACAGCACTACTTCTGCGCCCTTGTGTGATGATGACACTTGTCTATACAGC 660

Db 601 ATTTTACAGCACTACTTCTGCGCCCTTGTGTGATGATGACACTTGTCTATACAGC 660
 Oy 661 ATTTTACAGCACTACTTCTGCGCCCTTGTGTGATGATGACACTTGTCTATACAGC 720
 Db 661 ATTTTACAGCACTACTTCTGCGCCCTTGTGTGATGATGACACTTGTCTATACAGC 720
 Oy 721 AGGCTATACCACTTCTGCTACTCCCTTCATTTAGTATGTTTATACCTTCATATCTG 780
 Db 721 AGGCTATACCACTTCTGCTACTCCCTTCATTTAGTATGTTTATACCTTCATATCTG 780
 Oy 781 AGGCTATACCACTTCTGCTACTCCCTTCATTTAGTATGTTTATACCTTCATATCTG 840
 Db 781 AGGCTATACCACTTCTGCTACTCCCTTCATTTAGTATGTTTATACCTTCATATCTG 840
 Oy 841 CATGAAAGCTTATGTTTCTGACCATTAAGTGTCTGCAACACCTTGTGTAACCTGTTA 900
 Db 841 CATGAAAGCTTATGTTTCTGACCATTAAGTGTCTGCAACACCTTGTGTAACCTGTTA 900
 Oy 901 CTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 Db 901 CTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960
 Oy 961 GTAAGCGGGAACCTTGAAGCAACAAAGAAATTAAGTACTCAAAACACCTTGA 1014
 Db 961 GTAAGCGGGAACCTTGAAGCAACAAAGAAATTAAGTACTCAAAACACCTTGA 1014
 RESULT 8
 ABL56197
 ID ABL56197 standard; cDNA; 1288 BP.
 XX
 AC ABL56197;
 DT 05-JUL-2002 (first entry)
 XX
 DE Human P2Y1-11 encoding cDNA.
 XX
 KW Human, P2Y1-11; chromosome 13; G protein-coupled; receptor;
 KW gene therapy; thyroid; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 18..1031
 FT /tag a "P2Y1-like purine receptor"
 FT /product-
 XX
 DE10046970-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 22-SEP-2000; 2000DE-1046970.
 XX
 PR 22-SEP-2000; 2000DE-1046970.
 XX
 PA (BRUE/) BRUESS M.
 PA (BOEN/) BOENISCH H.
 XX
 PI Brues M., Boenisch H.
 XX
 DR WPI: 2002-353329/39.
 DR P-PDB: ABB79438.
 XX
 PT New human P2Y11 gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 XX
 PS Claim 5; Page 3; 5pp; German.
 XX
 CC The invention relates to the human P2Y11 gene (I), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies

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DB 8309 ATGAAATGAGCCACTAATATTTAGCAAAAGCTTCGATTTCCCGGATTTATGAGAGCTGCT 8368
OY 61 TTTGAAATTTGCATGATGAAATATCCCACTGAATGACATACCTCCCTGATATTTAT 120
DB 8369 TTTGAAATTTGCATGATGAAATATCCCACTGAATGACATACCTCCCTGATATTTAT 8428
OY 121 GGCATTTATCTTCCCTGATGATTTCCAGCAATGATGATGATGATGATGATGATGATGAT 180
DB 8429 GGCATTTATCTTCCCTGATGATTTCCAGCAATGATGATGATGATGATGATGATGATGAT 8488
OY 181 AAAATGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 8489 AAAATGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8548
OY 241 CTTGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 8549 CTTGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8608
OY 301 TTTGAGATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 8609 TTTGAGATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8668
OY 361 ATTCCTTCTCCTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 8669 ATTCCTTCTCCTACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8728
OY 421 TCGTTTTCATTTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 8729 TCGTTTTCATTTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8788
OY 481 TCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 8789 TCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8848
OY 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 8849 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8908
OY 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 8909 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8968
OY 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 8969 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9028
OY 721 AGGCTAACCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 9029 AGGCTAACCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9088
OY 781 AGGCTAACCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 9089 AGGCTAACCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9148
OY 841 CATTGAAGCTTAACTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 9149 CATTGAAGCTTAACTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9208
OY 901 CTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 9209 CTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9268
OY 961 GTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
DB 9269 GTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9322

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RESULT 11
 AAS08362
 ID AAS08362 standard; cdna; 1729 BP.
 XX
 AC AAS08362:

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XX 26-SEP-2001 (first entry)
XX Human cDNA encoding G-protein coupled receptor, GPCR 39404.
DE Human; G-protein coupled receptor; GPCR; 39404; immunogen; antibody;
XX Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;
KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
KW systemic lupus erythematosus; actinic keratosis; myocarditis;
KW Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasia;
KW inflammations; teratoma; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 294..1307
FT /tag="a
FT /product="Protein. 39404"
XX MO200149847-A2.
XX 12-JUL-2001.
XX 22-DEC-2000; 2000MO-US35309.
XX 30-DEC-1999; 99US-0475790.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, White D;
XX WPI: 2001-432880/46.
XX P-PSDB; AA004584.
XX Novel isolated 26904, 38911 and 39404 polypeptides which are seven
XX transmembrane proteins belonging to superfamily of G-protein-coupled
XX PT receptors, useful for treating disorders of spleen, lung, liver, brain
XX PT and kidney -
XX
XX Claim 2; Fig 1; 164pp; English.
XX
XX The sequence encodes a novel human seven transmembrane domain
XX protein belonging to the G-protein coupled receptor (GPCR) superfamily,
XX protein 39404. The receptor is useful in drug screening assays, to
XX identify compounds that modulate receptor activity and/or interact with
XX the receptor, and for producing antibodies specific for the receptor, its
XX regions or fragments. The receptor is useful for treating/diagnosing a
XX 26904, 38911 and 39404 protein-associated disorder characterised by
XX aberrant expression or activity of the protein, for monitoring
XX therapeutic effect during clinical trials and other treatment, as bait
XX proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
XX analysis. The proteins and nucleic acids encoding them are useful for
XX diagnosis and treatment of disorders selected from disorders of the
XX spleen, lung such as Good pasture's syndrome, liver such as viral
XX hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
XX such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
XX disease, colon such as Crohn's disease, uterus and endometrium such as
XX endometriosis, T-cell disorders such as systemic lupus erythematosus,
XX diseases of the skin such as actinic keratosis, disorders of the heart
XX CC such as myocarditis, disorders involving the thymus such as Kawasaki
XX syndrome, disorders involving blood vessels such as DiGeorge syndrome,
XX disorders involving B-cells such as peripheral B-cell neoplasia,
XX CC disorders of the breast such as inflammations, and disorders involving
XX CC the testis and epididymis such as teratoma. Numerous examples of
XX each type of disorder are given in the specification.
XX
XX Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;
XX
XX Query Match 99.7%; Score 1010.8; DB 22; Length 1729;
XX Best local Similarity 99.8%; Pred. No. 8.2e-288;
XX Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ATGAAATGAGCCACTAATATTTAGCAAAATGCTTCGATTTCCCGGATTTATGAGAGCTGCT 60

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Db      294 ATGAATGAGCGCACTAGACTTATGCAAAAGCTTCATATCCCGGATATGACGCT 353
Qy      61 TTTGGAATTTGCACTGATGAAATCATCCACTCAAGATGACATCCGCTTATTTAT 120
Db      354 TTTGGAATTTGCACTGATGAAATCATCCACTCAAGATGACATCCGCTTATTTAT 413
Qy      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCAATGATATGATATCACTTATTC 180
Db      414 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCAATGATATGATATCACTTATTC 473
Qy      181 AAAATGAGACCTTTGGAAGACAGACATATATGCTGAACCTGGCTGCACAGATCTG 240
Db      474 AAAATGAGACCTTTGGAAGACAGACATATATGCTGAACCTGGCTGCACAGATCTG 533
Qy      241 CTGATCTGACGACGCGCCCTCCCTGATTCACACATATGCAATGGCGAAAATGATC 300
Db      534 CTGATCTGACGACGCGCCCTCCCTGATTCACACATATGCAATGGCGAAAATGATC 593
Qy      301 TTTGGAATTTGCACTGATGAAATCATCCACTCAAGATGACATCCGCTTATTTAT 360
Db      594 TTTGGAATTTGCACTGATGAAATCATCCACTCAAGATGACATCCGCTTATTTAT 653
Qy      361 ATCCTCTCTCACTGCTTTCAGCATCTCCGCTACTGCTGATCATTTCAACCCATGAC 420
Db      654 ATCCTCTCTCACTGCTTTCAGCATCTCCGCTACTGCTGATCATTTCAACCCATGAC 713
Qy      421 TGCCTTTCCATTCACAAAACCTCGATGTCAGTTGATGACCTGCTGCTGCTGATTC 480
Db      714 TGCCTTTCCATTCACAAAACCTCGATGTCAGTTGATGACCTGCTGCTGCTGATTC 773
Qy      481 TCATGCTAGCTGCTGATGTCAGTACCTGCTGATGTCAGTACCTGCTGCTGATTC 540
Db      774 TCATGCTAGCTGCTGATGTCAGTACCTGCTGATGTCAGTACCTGCTGCTGATTC 833
Qy      541 TCAAGCTGCTGCACTGACACATTCGATGTCAGTACCTGCTGATGTCAGTACCTG 600
Db      834 TCAAGCTGCTGCACTGACACATTCGATGTCAGTACCTGCTGATGTCAGTACCTG 893
Qy      601 ATTTGACCTGCACTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      894 ATTTGACCTGCACTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953
Qy      661 ATTATCCACTGCTGACCAATGACATGCAAACTGACATGCTGCTGCTGCTGCTG 720
Db      954 ATTATCCACTGCTGACCAATGACATGCAAACTGACATGCTGCTGCTGCTGCTG 1013
Qy      721 AGGCTAACACTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db      1014 AGGCTAACACTTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1073
Qy      781 AGGCTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db      1074 AGGCTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1133
Qy      841 CATGACCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db      1134 CATGACCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1193
Qy      901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      1194 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
Qy      961 GTAAGCGGGAACCTTGAGCAAGCAAAATTTAGTACTAAACACCTTTGA 1014
Db      1254 GTAAGCGGGAACCTTGAGCAAGCAAAATTTAGTACTAAACACCTTTGA 1307

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RESULT 12
 ABV24026
 ID ABV24026 standard; cdna; 1729 BP.
 XX
 AC ABV24026;

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XX      16-SEP-2002 (first entry)
Dt      Human prostate expression marker cDNA 24017.
XX
DE      Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
Km      pharmacogenomic marker; gene; ss.
KW      Homo sapiens.
XX
OS      Homo sapiens.
XX
PN      WO200160860-A2.
XX
PD      23-AUG-2001.
XX
PF      20-FEB-2001; 2001MO-US05171.
XX
PR      17-FEB-2000; 2000US-183319P.
XX
PR      16-MAR-2000; 2000US-189862P.
XX
PR      25-MAY-2000; 2000US-207454P.
XX
PR      09-JUN-2000; 2000US-211314P.
XX
PR      18-JUL-2000; 2000US-219007P.
XX
PR      13-DEC-2000; 2000US-255281P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI      Schlegel R, Endege WO, Monahan JE.
XX
DR      WPI; 2001-662795/76.
XX
PT      Novel isolated nucleic acid molecule associated with cancerous state of
Pt      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS      Claim 1; Page 4453-4454; 11750pp; English.
XX
CC      The invention relates to an isolated nucleic acid molecule (I) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (I) is useful for:
CC      (a) assessing whether a patient is afflicted with prostate cancer;
CC      (b) monitoring the progression of prostate cancer in a patient;
CC      (c) assessing the efficacy of a test compound to inhibit prostate
CC      cancer in a patient;
CC      (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC      in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound;
CC      (g) determining whether prostate cancer has metastasized in a patient;
CC      (h) assessing the aggressiveness or indolence of prostate cancer in a
CC      patient;
CC      (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ      Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
XX
Query Match          99.7%; Score 1010.8; DB 23; Length 1729;
Best Local Similarity 99.8%; Pred. No. 8.2e-288;
Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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Qy      1 ATGAATGAGCGCACTAGACTTATGCAAAAGCTTCATATCCCGGATATGACGCT 60
Db      294 ATGAATGAGCGCACTAGACTTATGCAAAAGCTTCATATCCCGGATATGACGCT 353
Qy      61 TTTGGAATTTGCACTGATGAAATCATCCACTCAAGATGACATCCGCTTATTTAT 120
Db      354 TTTGGAATTTGCACTGATGAAATCATCCACTCAAGATGACATCCGCTTATTTAT 413
Qy      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCAATGATATGATATCACTTATTC 180
Db      414 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCAATGATATGATATCACTTATTC 473
Qy      181 AAAATGAGACCTTTGGAAGACAGACATATATGCTGAACCTGGCTGCACAGATCTG 240
Db      474 AAAATGAGACCTTTGGAAGACAGACATATATGCTGAACCTGGCTGCACAGATCTG 533

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QY 241 CTGTATCTGACAGCCCTCCCTTCCTGATTCATCTATGAGCAGTGGCGAAACTGGATC 300
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 Db 534 CTGTATCTGACAGCCCTCCCTTCCTGATTCATCTATGAGCAGTGGCGAAACTGGATC 593
 QY 301 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 360
 |||||||
 Db 594 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 653
 QY 361 ATCCCTCTCCCTACCGCTTCAGATCTCCGCTACGCTGTGATGATTCACCCATAGC 420
 |||||||
 Db 654 ATCCCTCTCCCTACCGCTTCAGATCTCCGCTACGCTGTGATGATTCACCCATAGC 713
 QY 421 TGCCTTTCATTCACAAAACCTGATGTGAGTTGATGATGATGATGATGATGATGATGAT 480
 |||||||
 Db 714 TGCCTTTCATTCACAAAACCTGATGTGAGTTGATGATGATGATGATGATGATGATGAT 773
 QY 481 TCAGCTGTACCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 |||||||
 Db 774 TCAGCTGTACCTGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
 QY 541 TCAGCTGTCTGACCTGACCTGACCTGATGATGATGATGATGATGATGATGATGATGAT 600
 |||||||
 Db 834 TCAGCTGTCTGACCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893
 QY 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 |||||||
 Db 894 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 953
 QY 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 |||||||
 Db 954 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1013
 QY 721 AGGCTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 |||||||
 Db 1014 AGGCTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1073
 QY 781 AGGCTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 |||||||
 Db 1074 AGGCTAACATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1133
 QY 841 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 |||||||
 Db 1134 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1193
 QY 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 |||||||
 Db 1194 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
 QY 961 GTTAAGCGGAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1014
 |||||||
 Db 1254 GTTAAGCGGAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1307
 RESULTE 13
 ABV25767
 ID ABV25767 standard; cDNA: 1729 BP.
 XX ABV25767;
 AC
 XX 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25758.
 XX
 KM Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-0505171.

XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JR;
 XX
 DR WPL; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 5175-5176; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
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 QY 1 ATGAATGAGCCACTAGACTTATGCAAAAGCTTCGATTTCCCGGATATGACAGCTGCT 60
 Db 294 ATGAATGAGCCACTAGACTTATGCAAAAGCTTCGATTTCCCGGATATGACAGCTGCT 353
 QY 61 TTGGAAATGCACTGATGAAACATCCGCTCAAGATGACATGACCTGTTATTTAT 120
 Db 354 TTGGAAATGCACTGATGAAACATCCGCTCAAGATGACATGACCTGTTATTTAT 413
 QY 121 GGCATATCTTCCCTGCGGATTTCCAGGCAATGACATGATGATGATGATGATGATGATGAT 180
 Db 414 GGCATATCTTCCCTGCGGATTTCCAGGCAATGACATGATGATGATGATGATGATGATGAT 473
 QY 181 AAATGAGACCTTGAAGAGACAGCAGCATATATGCTGAACCTGCTCAGAGATCTG 240
 Db 474 AAATGAGACCTTGAAGAGACAGCAGCATATATGCTGAACCTGCTCAGAGATCTG 533
 QY 241 CTGTATCTGACAGCCCTCCCTTCCTGATTCATGATGATGATGATGATGATGATGATGATGAT 300
 Db 534 CTGTATCTGACAGCCCTCCCTTCCTGATTCATGATGATGATGATGATGATGATGATGATGAT 593
 QY 301 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 360
 Db 594 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 653
 QY 361 ATCCCTCTCCCTACCGCTTCAGATCTCCGCTACGCTGTGATGATGATGATGATGATGATGAT 420
 Db 654 ATCCCTCTCCCTACCGCTTCAGATCTCCGCTACGCTGTGATGATGATGATGATGATGATGAT 713
 QY 421 TGCCTTTCATTCACAAAACCTGATGTGAGTTGATGATGATGATGATGATGATGATGATGAT 480
 Db 714 TGCCTTTCATTCACAAAACCTGATGTGAGTTGATGATGATGATGATGATGATGATGATGAT 773

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Db 954 ATTATCAACACTGTGACCCAGTGTGACGTAAGTGTGCTTAAAGCAGAAAGCAGCA 1013
 Qy 721 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 780
 Db 1014 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1073
 Qy 781 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 840
 Db 1074 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1133
 Qy 841 CATGAAGCTTACATGTTTCTGACATTTAGTGTCTGTAACACCTTTGGTAACCTGTTA 900
 Db 1134 CATGAAGCTTACATGTTTCTGACATTTAGTGTCTGTAACACCTTTGGTAACCTGTTA 1193
 Qy 901 CTATATGTGTGTGTCAGCAGCAACTTTCAGCAGGCTGTCTGCTCAACAGTGAAGCAAA 960
 Db 1194 CTATATGTGTGTGTCAGCAGCAACTTTCAGCAGGCTGTCTGCTCAACAGTGAAGCAAA 1253
 Qy 961 GTTACGGGAACTTGTGACGACCAAGAAATTAAGTACTCAAAACACCTTGA 1014
 Db 1254 GTTACGGGAACTTGTGACGACCAAGAAATTAAGTACTCAAAACACCTTGA 1307

RESULT 15

ID ABV30024 standard; cDNA; 1729 BP.
 ID ABV30024

AC ABV30024;

DT 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 30015.

KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KM pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN WO200160860-A2.

XX 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

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XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PA Schlegel R, Endege WO, Monahan JE;

PI MPI; 2001-662795/76.

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PT for detecting presence of prostate cancer, stage of prostate cancer

XX Claim 1; Page 6487-6488; 11750pp; English.

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Qy 1 ATGAATGAGCCACTAGACTATTATGCAAAATGCTTGTGATTTCCCGATATGACAGTGT 60
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 Qy 61 TTTGGAAATTTGACATGATGAAAACATCCCATCAAGATGACATCTCCCTGTATTTAT 120
 Db 354 TTTGGAAATTTGACATGATGAAAACATCCCATCAAGATGACATCTCCCTGTATTTAT 413
 Qy 121 GGCATATCTTCTCTGTTGGGATTTCCAGGCAATGAGTGTGATATCCACTATATTTTC 180
 Db 414 GGCATATCTTCTCTGTTGGGATTTCCAGGCAATGAGTGTGATATCCACTATATTTTC 473
 Qy 181 AAAATGAGACTTGGAAAGAGCAGACCATATATGCTGATGACCTGCTGACAGATCTG 240
 Db 474 AAAATGAGACTTGGAAAGAGCAGACCATATATGCTGATGACCTGCTGACAGATCTG 533
 Qy 241 CTGTATCTGACAGCCTCCCTCTCTGATTCATCTACTATGACAGTGGCAAACTGTGATC 300
 Db 534 CTGTATCTGACAGCCTCCCTCTCTGATTCATCTACTATGACAGTGGCAAACTGTGATC 593
 Qy 301 TTTGGAGATTTATGATGATGATTTATGCTTCACTGATTTCACTTCACTGATATACAG 360
 Db 594 TTTGGAGATTTATGATGATGATTTATGCTTCACTGATTTCACTTCACTGATATACAG 653
 Qy 361 ATCCCTTCTCCTACCTGTTTCAAGCATCTTCCCTGATCTGTGATGATCACTTCACTGAT 420
 Db 654 ATCCCTTCTCCTACCTGTTTCAAGCATCTTCCCTGATCTGTGATGATCACTTCACTGAT 713
 Qy 421 TGCCTTTTCCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 714 TGCCTTTTCCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGAT 773
 Qy 481 TCACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 774 TCACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 833
 Qy 541 TCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 834 TCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893
 Qy 601 ATTTGACATGCACTTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 Db 894 ATTTGACATGCACTTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
 Qy 661 ATTTGACATGCACTTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 954 ATTTGACATGCACTTCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
 Qy 721 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 780
 Db 1014 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1073
 Qy 781 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 840
 Db 1074 AGGCTAACATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1133
 Qy 841 CATGAAGCTTACATGTTTCTGACATTTAGTGTCTGTAACACCTTTGGTAACCTGTTA 900
 Db 1134 CATGAAGCTTACATGTTTCTGACATTTAGTGTCTGTAACACCTTTGGTAACCTGTTA 1193
 Qy 901 CTATATGTGTGTGTCAGCAGCAACTTTCAGCAGGCTGTCTGCTCAACAGTGAAGCAAA 960

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Db	1194	CTATATGTGTGTGCACGACACTTTCAGCGCTGTCTCACAAGAGAGCAA	1253
Qy	961	GTAAGCGGAGACTTGAAGCAAGAAATTAAGTTACTCAACACACCTTGA	1014
Db	1254	GTAAGCGGAGACTTGAAGCAAGAAATTAAGTTACTCAACACACCTTGA	1307

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 Job time : 306 secs

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